

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 15:03:41 ; Search time 79 Seconds
(without alignments)
1552.980 Million cell updates/sec

Title: US-09-401-636-8

Perfect score: 1856

Sequence: 1 EFHHHHHTLSLPESGPVTI.....HEALPGSRTLEKSLHYSAGN 342

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 1640122

Minimum DB seq length: 0
Maximum DB seq length: 342

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23sep04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1856	100.0	342	3 AAB06205	Immunogen
2	1786	96.2	338	8 ADF90025	Opossum-h
3	1786	96.2	338	8 ADN00646	OSO prote
4	1644.5	88.6	341	3 AAB06208	Immunogen
5	1584.5	85.4	341	3 AAB03644	Opossum I
6	1568.5	84.5	341	3 AAB06206	Immunogen
7	1498.5	80.7	337	8 ADF90022	Opossum-r
8	1498.5	80.7	337	8 ADN00643	ORO prote
9	1392.5	75.0	341	3 AAB06202	Immunogen
10	1375	74.1	342	3 AAB06201	Immunogen
11	1038.5	56.0	320	6 AAO19667	Human IGE
12	1038.5	56.0	323	5 AAU80286	Human IGE
13	1038.5	56.0	323	5 AAU80285	Human IGE
14	1038.5	56.0	323	5 AAU80284	Human IGE
15	1038.5	56.0	324	2 AAR32559	Fc(epsilo
16	1038.5	56.0	325	2 AAR75225	Human IGE
17	1038.5	56.0	325	2 AAR77241	Human IGE
18	1038.5	56.0	331	3 AAB03642	Human IGE
19	1038.5	56.0	331	7 ADD25768	Binding d
20	1036.5	55.8	330	5 AAU80289	Human IGE
21	1035.5	55.8	325	3 AAY79994	Human imm
22	1034.5	55.7	326	5 AAU80288	Human IGE
23	1019.5	54.9	325	2 AAR55582	Fc(epsilo
24	1019.5	54.9	325	2 AAR3582	CH2 to CH
25	961	51.8	312	3 AAY79995	Dog immun

26	795.5	42.9	201	2 AAR85589	Fc(epsilo
27	791.5	42.6	220	8 ADL01587	Human mut
28	779.5	42.0	223	8 ADL01584	Human imm
29	778.5	41.9	218	2 AAR85583	Fc(epsilo
30	778.5	41.9	220	8 ADL01589	Human mut
31	778.5	41.9	222	4 ABP60380	Human IGE
32	778.5	41.9	222	4 AAG65599	Amino aci
33	778.5	41.9	222	8 ADL01578	Human imm
34	777.5	41.9	220	8 ADL01593	Human mut
35	777.5	41.9	220	8 ADL01603	Human mut
36	774.5	41.7	220	8 ADL01599	Human mut
37	773.5	41.7	220	8 ADL01601	Human mut
38	773.5	41.7	220	8 ADL01595	Human mut
39	773.5	41.7	220	8 ADL01591	Human mut
40	772.5	41.6	220	8 ADL01597	Human mut
41	767.5	41.4	340	3 AAB03643	Rat IGE h
42	746.5	40.2	332	5 AAU80298	Murine Ig
43	746.5	40.2	332	5 AAU80299	Murine Ig
44	746.5	40.2	332	5 AAU80297	Mouse IGE
45	728.5	39.3	313	3 AAY79996	Rat immun

ALIGNMENTS

RESULT 1
AAB06205
ID AAB06205 standard; protein; 342 AA.
XX AAB06205;
AC AAB06205;
XX
DT 12-SEP-2003 (revised)
DT 22-NOV-2000 (first entry)
XX
DE Immunogenic peptide consisting of opossum CH2, human CH3 and opossum CH4.
XX Human; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;
KW asthma; eczema; immunogenic peptide.
XX
OS Didelphis virginiana.
OS Homo sapiens.
OS Chimeric.
XX
PN WO200025722-A2.
XX
PD 11-MAY-2000.
XX
PF 21-OCT-1999; 99WO-SE001896.
XX
PR 02-NOV-1998; 98US-0106652P.
XX 22-SEP-1999; 99US-00401636.
PA (RESI-) RESISTENTIA PHARM AB.
PI Hellman LT;
XX
DR WPI; 2000-365342/31.
XX
PT Immunogenic polypeptides useful for preventing the harmful effects of immunoglobulin E in mammals.
PS Disclosure; Fig 2; 50pp; English.
XX
CC The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2 and 4 of the opossum IgE and the heavy chain constant region 3 from the human. It was shown to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema.
CC (Updated on 12-SEP-2003 to standardise OS field)

SQ Sequence 342 AA;
 Query Match 100.0%; Score 1856; DB 3; Length 342;
 Best Local Similarity 100.0%; Pred. No. 5.4e-146;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHHHHHTLSLSPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHVHTW 60
 DB 1 EHHHHHTLSLSPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHVHTW 60

QY 61 LVDGQAEALFPYTRPKREGGQTSLSQSEVNIQTQWMSNTYTCHVKHNGSIFEDSSR 120
 DB 61 LVDGQAEALFPYTRPKREGGQTSLSQSEVNIQTQWMSNTYTCHVKHNGSIFEDSSR 120

QY 121 KCADSNPRGVSAVLSRPSFDLFIKSPITICLVVDLAPSKGTVNLTSRASGKPVNHST 180
 DB 121 KCADSNPRGVSAVLSRPSFDLFIKSPITICLVVDLAPSKGTVNLTSRASGKPVNHST 180

QY 181 RXEEKORNGTLVTSPLPVGTRDWIEGETYQCRVTHPLPALMRSTTKLPCKRLAPEVY 240
 DB 181 RXEEKORNGTLVTSPLPVGTRDWIEGETYQCRVTHPLPALMRSTTKLPCKRLAPEVY 240

QY 241 MLPPSPETGTRTVTCLIRGYPSEISVQWLPNNEEDHTGHHTTRPKQKHGTDPSFFL 300
 DB 241 MLPPSPETGTRTVTCLIRGYPSEISVQWLPNNEEDHTGHHTTRPKQKHGTDPSFFL 300

QY 301 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342
 DB 301 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342

RESULT 2
 ADF90025
 ID ADF90025 standard; protein; 338 AA.
 AC ADF90025;
 XX
 XX 26-FEB-2004 (first entry)
 DT
 XX Opossum-human chimeric IgE polypeptide.
 DE
 XX IgE; immunoglobulin; antibody; opossum; human; vaccine; antiallergic;
 KW antidiathmatic; dermatological.
 KW
 XX Chimeric.
 OS
 XX Didelphis virginiana.
 OS
 XX Homo sapiens.
 XX
 PN WO2003096966-A2.
 XX
 XX 27-NOV-2003.
 PD
 XX
 XX 15-MAY-2003; 2003WO-IB002503.
 PF
 XX
 XX 21-MAY-2002; 2002US-0382552P.
 PR
 XX
 XX (RESI-) RESISTENTIA PHARM AB.
 PA
 XX
 XX Lundgren M, Fuentes A, Magnusson A;
 PI
 XX WPI; 2004-042496/04.
 DR
 DR N-PSDB; ADF90024, ADF90023.
 XX
 XX New host cell comprising a nucleic acid vector comprising a
 PT cytomegalovirus promoter, an Ig leader sequence, an insert sequence or
 PT SV40 late polyadenylation sequence, useful in producing a chimeric IgE
 PT polypeptide.
 PT
 XX
 XX Claim 3; SEQ ID NO 6; 23pp; English.
 PS
 XX
 XX The present sequence is the protein sequence of an opossum CH2-human CH3-
 CC opossum CH4 (OSO) chimeric IgE polypeptide. A vector comprising DNA
 CC encoding OSO can be used for recombinant production this chimeric IgE in

CC host, e.g. CHO, cells. The invention provides methods and materials
 CC related to expressing chimeric IgE proteins. Nucleic acid vectors, host
 CC cells, and methods for producing chimeric IgE polypeptides are provided.
 CC When administered to a mammal, the chimeric polypeptides can reduce the
 CC IGE antibody effects of IgE-related diseases such as asthma, allergies
 CC and eczema.
 XX
 SQ Sequence 338 AA;
 Query Match 96.2%; Score 1786; DB 8; Length 338;
 Best Local Similarity 99.4%; Pred. No. 3.6e-140;
 Matches 334; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 9 TLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHVHTWLDQGEAE 68
 DB 3 TLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHVHTWLDQGEAE 62

QY 69 NLPFYTRPKREGGQTSLSQSEVNIQTQWMSNTYTCHVKHNGSIFEDSSRKCADSNPR 128
 DB 63 NLPFYTRPKREGGQTSLSQSEVNIQTQWMSNTYTCHVKHNGSIFEDSSRKCADSNPR 122

QY 129 GVSAYLSRSPSPDLFIKSPITICLVVDLAPSKGTVNLTSRASGKPVNHSTRKKEKQSN 188
 DB 123 GVSAYLSRSPSPDLFIKSPITICLVVDLAPSKGTVNLTSRASGKPVNHSTRKKEKQSN 182

QY 189 GTLTVTSTLPVGTTRDWIEGETYQCRVTHPLPALMRSTTKL--PGKRLAPEVYMLPPSP 246
 DB 183 GTLTVTSTLPVGTTRDWIEGETYQCRVTHPLPALMRSTTKLASPGKRLAPEVYMLPPSP 242

QY 247 EETGTRTVTCLIRGYPSEISVQWLPNNEEDHTGHHTTRPKQKHGTDPSFLSRMLV 306
 DB 243 EETGTRTVTCLIRGYPSEISVQWLPNNEEDHTGHHTTRPKQKHGTDPSFLSRMLV 302

QY 307 NKSIMEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342
 DB 303 NKSIMEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 338

RESULT 3
 ADF90046
 ID ADF90046 standard; protein; 338 AA.
 AC ADF90046;
 XX
 XX 17-JUN-2004 (first entry)
 DT
 XX OSO protein, SEQ ID 6.
 DE
 XX Antiallergic; Vaccine; self-IgE; OSO; allergy.
 KW
 XX Synthetic.
 OS
 XX WO2004022094-A1.
 PN
 XX 18-MAR-2004.
 PD
 XX
 XX 02-JUN-2003; 2003WO-IB003075.
 PF
 XX
 XX 05-SEP-2002; 2002US-0408648P.
 PR
 XX (RESI-) RESISTENTIA PHARM AB.
 PA
 XX
 XX Hellman LT, Persson S, Gansson A;
 PI
 XX WPI; 2004-248376/23.
 DR
 DR N-PSDB; ADF90045.
 XX
 XX New composition comprising a self-IgE polypeptide and an aluminum
 PT compound, useful for inducing an anti self-IgE antibody response in a
 PT mammal for treating or preventing allergies.
 PT
 XX
 XX Claim 3; Fig 8; 102pp; English.
 PS
 XX

CC The present invention relates to a composition comprising a polypeptide
CC and an aluminum compound, where the polypeptide comprises a self-IgE
CC polypeptide sequence (e.g. an ORO polypeptide or an OSO polypeptide;
CC ADN00643, ADN00646, ADN00650, ADN00652, ADN00654, ADN00656, ADN00658 or
CC ADN00661). Administration of the composition to a mammal reduces the
CC level of detectable free IgE in the mammal. The composition is useful for
CC inducing an anti self-IgE antibody response in a mammal for treating or
CC preventing allergies. The present sequence is an OSO protein, used to
CC illustrate the invention. The OSO protein contains an opossum CH2 IgE
CC domain followed by a human CH3 IgE domain followed by an opossum CH4 IgE
CC domain.

XX SQ Sequence 338 AA;
XX
XX Query Match 96.2%; Score 1786; DB 8; Length 338;
XX Best Local Similarity 99.4%; Pred. No. 3 6e-140; Indels 2; Gaps 1;
XX Matches 334; Conservative 0; Mismatches 0; Mismatches 0; Indels 2; Gaps 1;

QY 9 TISLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTVWLVDQAE 68
Db 3 TISLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTVWLVDQAE 62
QY 69 NUFFPYTRKREGGQTFSLQSEVNITQGMMSNTYTCHVKNGSTIFEDSSRKCADSNPR 128
Db 63 NUFFPYTRKREGGQTFSLQSEVNITQGMMSNTYTCHVKNGSTIFEDSSRKCADSNPR 122
QY 129 GVSAYLSRSPDFLIRKSPPTITCLVVDLAPSKGTVNLTWASRSGKPVNHSRKEKQRN 188
Db 123 GVSAYLSRSPDFLIRKSPPTITCLVVDLAPSKGTVNLTWASRSGKPVNHSRKEKQRN 182
QY 189 GILTVTSTLPVGTQWIEGTQCRVTHPHLPRALMRSTTKL--PGKRLAPEVYMLPSP 246
Db 183 GILTVTSTLPVGTQWIEGTQCRVTHPHLPRALMRSTTKLASPGKRLAPEVYMLPSP 242
QY 247 EETGTRTTCVLCIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFLLYRMLV 306
Db 243 EETGTRTTCVLCIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFLLYRMLV 302
QY 307 NKSIVKGNLVCVHVHEALPGSRTLEKSLHYSAGN 342
Db 303 NKSIVKGNLVCVHVHEALPGSRTLEKSLHYSAGN 338

RESULT 4
AAB06208
ID AAB06208 standard; protein; 341 AA.
XX
XX AAB06208;
XX
XX 12-SEP-2003 (revised)
DT 22-NOV-2000 (first entry)
XX
XX Immunogenic peptide consisting of opossum CH2, dog CH3 and opossum CH4.
DE
XX Dog; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;
KW asthma; eczema; immunogenic peptide.
XX
XX Didelphis virginiana.
OS
OS Canis sp.
OS Chimeric.
XX
XX WO2000025722-A2.
XX
XX 11-MAY-2000.
XX
XX 21-OCT-1999; 99WO-SE001896.
XX
XX 02-NOV-1998; 98US-0106652P.
PR 22-SEP-1999; 99US-00401636.
XX
XX (RESI-) RESISTENTIA PHARM AB.
PA
XX Hellman LT;
PI

XX WPI; 2000-365342/31.
DR
XX Immunogenic polypeptides useful for preventing the harmful effects of
XX immunoglobulin E in mammals.
PT
XX Disclosure; Fig 2; 50pp; English.

XX The present sequence is an immunogenic peptide consisting of the heavy
CC chain constant regions 2 and 4 of the opossum IgE and the heavy chain
CC constant region 3 from the dog. It was shown to cause a stronger
CC polyclonal anti-self IgE response than peptides consisting of the same
CC regions from one mammal. Immunogenic peptides, particularly those
CC consisting of different heavy chain constant regions, can be used for
CC vaccination in humans, against bacterial and viral infections and
CC allergies, such as asthma, fur, pollen and food allergies and eczema.
CC (Updated on 12-SEP-2003 to standardise OS field)

XX SQ Sequence 341 AA;
XX
XX Query Match 88.6%; Score 1644.5; DB 3; Length 341;
XX Best Local Similarity 88.0%; Pred. No. 2.2e-128; Indels 1; Gaps 1;
XX Matches 301; Conservative 17; Mismatches 23; Indels 1; Gaps 1;

QY 1 EFHHHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTW 60
Db 1 EFHHHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTW 60
QY 61 LVDQAEANLFPYTRKREGGQTFSLQSEVNITQGMMSNTYTCHVKNGSTIFEDSSR 120
Db 61 LVDQAEANLFPYTRKREGGQTFSLQSEVNITQGMMSNTYTCHVKNGSTIFEDSSR 120
QY 121 KCADSNPRGVSAYLSRSPDFLIRKSPPTITCLVVDLAPSKGTVNLTWASRSGKPVNHS 180
Db 121 KCSESDPRGVTSLSPSPPLDLYVHKAPKITCLVVDLATWEG-MNLTWYRESKEPVNPGP 179
QY 181 RKEKQKNGTLTSTLPVGTQWIEGTQCRVTHPHLPRALMRSTTKLPGLAPEVY 240
Db 180 LNKDHFNGTITVTSTLPVNDWIEGTTCRVTHPHLPDILVRSIAKLPGLAPEVY 239
QY 241 MLPSPPEETGTRTTCVLCIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFLL 300
Db 240 MLPSPPEETGTRTTCVLCIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFLL 299
QY 301 YSRMLVKNKSWKGNLVCVHVHEALPGSRTLEKSLHYSAGN 342
Db 300 YSRMLVKNKSWKGNLVCVHVHEALPGSRTLEKSLHYSAGN 341

RESULT 5
AAB03644
ID AAB03644 standard; protein; 341 AA.
XX
XX AAB03644;
XX
XX 22-NOV-2000 (first entry)
DT
XX
XX Opossum IgE heavy chain constant regions 2, 3 and 4.
DE
XX Opossum; immunoglobulin E; IgE; vaccination; infection; allergy; asthma;
KW eczema; immunogenic peptide.
XX
XX Didelphis virginiana.
OS
XX WO2000025722-A2.
XX
XX 11-MAY-2000.
XX
XX 21-OCT-1999; 99WO-SE001896.
XX
XX 02-NOV-1998; 98US-0106652P.
PR 22-SEP-1999; 99US-00401636.
XX
XX

PA (RESI-) RESISTENTIA PHARM AB.
 XX Hellman LT;
 PI WPI; 2000-365342/31.
 DR
 XX Immunogenic polypeptides useful for preventing the harmful effects of
 PT immunoglobulin E in mammals.
 PT
 XX Disclosure; Fig 1; 50pp; English.
 PS
 XX The present sequence is an immunogenic peptide consisting of the heavy
 CC chain constant regions 2, 3 and 4 of the opossum IgE. It was used to
 CC construct a number of immunogenic peptides which consisted of regions of
 CC IgE from different mammals, which appear to cause a stronger polyclonal
 CC anti-self IgE response than peptides consisting of the same regions from
 CC one mammal. Immunogenic peptides, particularly those consisting of
 CC different heavy chain constant regions, can be used for vaccination in
 CC humans, against bacterial and viral infections and allergies, such as
 CC asthma, fur, pollen and food allergies and eczema
 CC
 XX Sequence 341 AA;
 SQ
 Query Match 85.4%; Score 1584.5; DB 3; Length 341;
 Best Local Similarity 85.1%; Pred. No. 2.2e-123;
 Matches 291; Conservative 22; Mismatches 28; Indels 1; Gaps 1;
 QY 1 EFFFFHHHTLSLSPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGSPAKVHTW 60
 DB 1 EFFFFHHHTLSLSPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGSPAKVHTW 60
 QY 61 LVDQQAENLFPYTRPKREGGQTFSLQSEVNTIQQWSSNTYTCHVKHNGSIFEDSSR 120
 DB 61 LVDQQAENLFPYTRPKREGGQTFSLQSEVNTIQQWSSNTYTCHVKHNGSIFEDSAQ 120
 QY 121 KCADSNPRGSAVLSRSPDFIRKSPITCLVLDLAPSKGTVNLTPWRSAGKPVNHST 180
 DB 121 KCSDTOPRGISAVILPPTQDLFVKKVTIGCLIVDLA-SAENVKVTWRSRSGGPNPSS 179
 QY 181 RKEKORNGTLTSTLPVGTDRWIEGTYQCRVTHPLPRALMRSTTKLPGRKLAPEVY 240
 DB 180 LVKQEQNGFTVTSLPNDTDWIEGTYTCRLSPDMPVPLIRIISKAPGRKLAPEVY 239
 QY 241 MLPPSPETGTTTRVTCCLINGFYPSBSIQWLFNNEEDHTGHTTTRPKQDHTDPSFFL 300
 DB 240 MLPPSPETGTTTRVTCCLINGFYPSBSIQWLFNNEEDHTGHTTTRPKQDHTDPSFFL 299
 QY 301 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342
 DB 300 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341
 RESULT 6
 AAB06206
 ID AAB06206 standard; protein; 341 AA.
 XX AAB06206;
 XX
 XX 12-SEP-2003 (revised)
 DT 22-NOV-2000 (first entry)
 XX
 XX Immunogenic peptide consisting of opossum CH2, rat CH3 and opossum CH4.
 XX Rat; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;
 KW asthma; eczema; immunogenic peptide.
 XX
 XX Didephis virginiana.
 OS Rattus sp.
 OS Chimeric.
 XX WO200025722-A2.
 FN
 XX 11-MAY-2000.
 PD

XX 21-OCT-1999; 99WO-SE001896.
 PF
 XX 02-NOV-1998; 98US-0106652P.
 PR
 XX 22-SEP-1999; 99US-00401636.
 XX
 XX (RESI-) RESISTENTIA PHARM AB.
 PA Hellman LT;
 PI WPI; 2000-365342/31.
 DR
 XX Immunogenic polypeptides useful for preventing the harmful effects of
 PT immunoglobulin E in mammals.
 PT
 XX Disclosure; Fig 2; 50pp; English.
 PS
 XX The present sequence is an immunogenic peptide consisting of the heavy
 CC chain constant regions 2 and 4 of the opossum IgE and the heavy chain
 CC constant region 3 from the rat. It was shown to cause a stronger
 CC polyclonal anti-self IgE response than peptides consisting of the same
 CC regions from one mammal. Immunogenic peptides, particularly those
 CC consisting of different heavy chain constant regions, can be used for
 CC vaccination in humans, against bacterial and viral infections and
 CC allergies, such as asthma, fur, pollen and food allergies and eczema.
 CC (Updated on 12-SEP-2003 to standardise OS field)
 CC
 XX Sequence 341 AA;
 SQ
 Query Match 84.5%; Score 1568.5; DB 3; Length 341;
 Best Local Similarity 83.3%; Pred. No. 4.6e-122;
 Matches 285; Conservative 20; Mismatches 36; Indels 1; Gaps 1;
 QY 1 EFFFFHHHTLSLSPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGSPAKVHTW 60
 DB 1 EFFFFHHHTLSLSPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGSPAKVHTW 60
 QY 61 LVDQQAENLFPYTRPKREGGQTFSLQSEVNTIQQWSSNTYTCHVKHNGSIFEDSSR 120
 DB 61 LVDQQAENLFPYTRPKREGGQTFSLQSEVNTIQQWSSNTYTCHVKHNGSIFEDSSR 120
 QY 121 KCADSNPRGSAVLSRSPDFIRKSPITCLVLDLAPSKGTVNLTPWRSAGKPVNHST 180
 DB 121 RCDDEPRGVITLIPSPDLIYENGTPKLTCLVLDL-ESEENITVTVWRKKSIGSAS 179
 QY 181 RKEKORNGTLTSTLPVGTDRWIEGTYQCRVTHPLPRALMRSTTKLPGRKLAPEVY 240
 DB 180 QRSTKHNATTSITLIPVDAKWIEGEGYQCRVDHPHPKPIVRGITKLPGRKLAPEVY 239
 QY 241 MLPPSPETGTTTRVTCCLINGFYPSBSIQWLFNNEEDHTGHTTTRPKQDHTDPSFFL 300
 DB 240 MLPPSPETGTTTRVTCCLINGFYPSBSIQWLFNNEEDHTGHTTTRPKQDHTDPSFFL 299
 QY 301 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342
 DB 300 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341
 RESULT 7
 ADF90022
 ID ADF90022 standard; protein; 337 AA.
 XX ADF90022;
 AC
 XX 26-FEB-2004 (first entry)
 DT
 XX Opossum-rat chimeric IgE polypeptide.
 DE
 XX IgE; immunoglobulin; antibody; opossum; rat; vaccine; antiallergic;
 KW antiasthmatic; dermatological.
 XX Chimeric.
 OS Didephis virginiana.
 OS

OS Rattus sp.
 XX WO2003036966-A2.
 XX 27-NOV-2003.
 XX 15-MAY-2003; 2003WO-IB002503.
 XX 21-MAY-2002; 2002US-0382552P.
 XX (RESI-) RESISTENTIA PHARM AB.
 XX Lundgren M, Fuentes A, Magnusson A;
 XX WPI; 2004-042496/04.
 XX N-PSDB; ADF90020, ADF90021.
 XX New host cell comprising a nucleic acid vector comprising a
 PT cytomegalovirus promoter, an Ig leader sequence, an insert sequence or
 PT SV40 late polyadenylation sequence, useful in producing a chimeric IgE
 PT polypeptide.
 XX
 PS Claim 3; SEQ ID NO 3; 23pp; English.
 XX
 CC The present sequence is the protein sequence of an opossum CH2-rat CH3-
 CC opoosum CH4 (ORO) chimeric IgE polypeptide. A vector comprising a nucleic
 CC acid encoding ORO can be used for recombinant production of this chimeric
 CC IgE in host, e.g. CHO, cells. The invention provides methods and
 CC materials related to expressing chimeric IgE proteins. Nucleic acid
 CC vectors, host cells, and methods for producing chimeric IgE polypeptides
 CC are provided. When administered to a mammal, the chimeric polypeptides
 CC can reduce the IgE antibody effects of IgE-related diseases such as
 CC asthma, allergies and eczema.
 XX
 SQ Sequence 337 AA;
 Query Match 80.7%; Score 1498.5; DB 8; Length 337;
 Best Local Similarity 82.4%; Pred. No. 3.1e-116;
 Matches 277; Conservative 20; Mismatches 36; Indels 3; Gaps 2;
 QY 9 TSLSPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTLVVDGQAE 68
 Db 3 TSLSPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTLVVDGQAE 62
 QY 69 NLFPTTRPKREGGQTFSLQSEVNITQGWMSNTYTCHVKNGSIFEDSSRCKADSNPR 128
 Db 63 NLFPTTRPKREGGQTFSLQSEVNITQGWMSNTYTCHVKNGSIFEDSSRCKADSNPR 122
 QY 129 GVSAYLSRSPFDLFIKSPFTITCLVVDLAPSKGTVNLTWASRASKPVNHSRKEEKORN 188
 Db 123 GVITLIPSPDLIYENGTPKLTCLVLDL-ESEENITVWREKKSIGASQSTKHNN 181
 QY 189 GTLTVTSTLPVGRDWIEGETYQCRVTHPLPALMRSTTKL--PGKRLAPEVYMLPPSP 246
 Db 182 ATTSITSLPVDADKIEGEGYQCRVDHPHFKPIVRSITKLASPGKRLAPEVYMLPPSP 241
 QY 247 EETGTRTITVCLIRGFPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFLYSRMLV 306
 Db 242 EETGTRTITVCLIRGFPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFLYSRMLV 301
 QY 307 NKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
 Db 302 NKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 337
 RESULT 8
 ADN00643
 ID ADN00643 standard; protein; 337 AA.
 XX
 AC ADN00643;
 XX
 DT 17-JUN-2004 (first entry)
 XX

DE ORO protein, SEQ ID 3.
 XX Antiallergic; Vaccine; self-IgE; ORO; OSO; allergy.
 XX Synthetic.
 OS
 XX WO2004022094-A1.
 XX 18-MAR-2004.
 XX 02-JUN-2003; 2003WO-IB003075.
 XX 05-SEP-2002; 2002US-0408648P.
 XX (RESI-) RESISTENTIA PHARM AB.
 XX Hellman LT, Persson S, Ganssion A;
 PI
 XX WPI; 2004-248376/23.
 DR N-PSDB; ADN00642.
 XX
 XX New composition comprising a self-IgE polypeptide and an aluminum
 PT compound, useful for inducing an anti self-IgE antibody response in a
 PT mammal for treating or preventing allergies.
 PT
 PS Claim 3; Fig 4; 102pp; English.
 XX
 CC The present invention relates to a composition comprising a polypeptide
 CC and an aluminum compound, where the polypeptide comprises a self-IgE
 CC polypeptide sequence (e.g. an ORO polypeptide or an OSO polypeptide;
 CC ADN00643, ADN00646, ADN00650, ADN00652, ADN00654, ADN00656, ADN00658 or
 CC ADN00661). Administration of the composition to a mammal reduces the
 CC level of detectable free IgE in the mammal. The composition is useful for
 CC inducing an anti self-IgE antibody response in a mammal for treating or
 CC preventing allergies. The present sequence is an ORO protein, used to
 CC illustrate the invention. The ORO protein contains an opoosum CH2 IgE
 CC domain followed by a rat CH3 IgE domain followed by an opoosum CH4 IgE
 CC domain.
 XX
 SQ Sequence 337 AA;
 Query Match 80.7%; Score 1498.5; DB 8; Length 337;
 Best Local Similarity 82.4%; Pred. No. 3.1e-116;
 Matches 277; Conservative 20; Mismatches 36; Indels 3; Gaps 2;
 QY 9 TSLSPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTLVVDGQAE 68
 Db 3 TSLSPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTLVVDGQAE 62
 QY 69 NLFPTTRPKREGGQTFSLQSEVNITQGWMSNTYTCHVKNGSIFEDSSRCKADSNPR 128
 Db 63 NLFPTTRPKREGGQTFSLQSEVNITQGWMSNTYTCHVKNGSIFEDSSRCKADSNPR 122
 QY 129 GVSAYLSRSPFDLFIKSPFTITCLVVDLAPSKGTVNLTWASRASKPVNHSRKEEKORN 188
 Db 123 GVITLIPSPDLIYENGTPKLTCLVLDL-ESEENITVWREKKSIGASQSTKHNN 181
 QY 189 GTLTVTSTLPVGRDWIEGETYQCRVTHPLPALMRSTTKL--PGKRLAPEVYMLPPSP 246
 Db 182 ATTSITSLPVDADKIEGEGYQCRVDHPHFKPIVRSITKLASPGKRLAPEVYMLPPSP 241
 QY 247 EETGTRTITVCLIRGFPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFLYSRMLV 306
 Db 242 EETGTRTITVCLIRGFPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFLYSRMLV 301
 QY 307 NKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
 Db 302 NKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 337
 RESULT 9
 AAB06202
 ID AAB06202 standard; protein; 341 AA.

XX AAB06202;
 XX 12-SEP-2003 (revised)
 XX 22-NOV-2000 (first entry)
 XX Immunogenic peptide consisting of opossum CH2, mouse CH3 and opossum CH4.
 XX Mouse; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;
 XX asthma; eczema; immunogenic peptide.
 XX Didelphis virginiana.
 XX Mus sp.
 XX Chimeric.
 XX Key Location/Qualifiers
 XX Misc-difference 1. 341
 XX /label= OTHER
 XX /note= "Xaa=unknown"
 XX WO200025722-A2.
 XX 11-MAY-2000.
 XX 21-OCT-1999; 99WO-SF001896.
 XX 02-NOV-1998; 98US-0106652P.
 XX 22-SEP-1999; 99US-00401636.
 XX (RESI-) RESISTENTIA PHARM AB.
 XX Hellman LT;
 XX WPI; 2000-365342/31.
 XX Immunogenic polypeptides useful for preventing the harmful effects of
 XX immunoglobulin E in mammals.
 XX Disclosure; Fig 2; 50pp; English.
 XX The present sequence is an immunogenic peptide consisting of the heavy
 XX chain constant regions 2 and 4 of the opossum IgE and the heavy chain
 XX constant region 3 from the mouse. It was shown to cause a stronger
 XX polyclonal anti-self IgE response than peptides consisting of the same
 XX regions from one mammal. Immunogenic peptides, particularly those
 XX consisting of different heavy chain constant regions, can be used for
 XX vaccination in humans, against bacterial and viral infections and
 XX allergies, such as asthma, fur, pollen and food allergies and eczema.
 XX (Updated on 12-SEP-2003 to standardise OS field)
 XX Sequence 341 AA;
 XX Query Match 75.0%; Score 1392.5; DB 3; Length 341;
 XX Best Local Similarity 76.7%; Pred. No. 2.1e-107;
 XX Matches 263; Conservative 22; Mismatches 53; Indels 5; Gaps 3;
 QY 1 EFHHHHHTLSLPESGPTVITPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW 60
 DB 1 EFHHHHHTLSLPESGPTVITPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW 60
 QY 61 LVDGQAEHLFPYTTTRPKREGGQTFSLQSEVNITQGWSSNTYTCHVKHNGSIFEDSSR 120
 DB 61 LVDGQAEHLFPYTTTRPKREGGQTFSLQSEVNITQGWSSNTYTCHVKHNGSIFEDSSR 120
 QY 121 KCADSNPRGVSAYLSRPSFDFIRKSPITCLVWDLPASKVTALTWASRAGKPVNHS 180
 DB 121 RCPDHPRGVITVILPSPDLVYQHCAPKLTCLVLDLSEK-HINVTWNQ--KPTXXXA 177
 QY 181 RK--EKQKNGTLVTSTLPVGTROMIEGETYOCRTVTHPLPALMRSTTKLPGRKLAPE 238
 DB 178 XQWYTKHHHATTTXITSLPVVXKDWIEGYXQIXDHPHPKIXXVSPITRPGKRLAPX 237
 QY 239 VYMLPPSPETGTRTTRVTCILRGFYSEISVQWLFNNEEDHTGHTTTRPQKHGDTXSF 298

DB 238 VYMLPPSPETGTRTTRVTCILRGFYSEISVQWLFNNEEDHTGHTTTRPQKHGDTXSF 297
 QY 299 FLYSRLVYKSIWEKGNLVTCTVWVHEALPGSRTLEKSLHYSAG 341
 DB 298 FLYSRLVYKSIWEKGNLVTCTVWVHEALPGSRTLEKSLHYSAG 340
 RESULT 10
 AAB06201
 ID AAB06201 standard; protein; 342 AA.
 XX AC AAB06201;
 XX 12-SEP-2003 (revised)
 XX 22-NOV-2000 (first entry)
 XX Immunogenic peptide consisting of opossum CH2, CH4 and rat/opossum CH3.
 XX Rat; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;
 XX asthma; eczema; immunogenic peptide.
 XX Didelphis virginiana.
 XX Rattus sp.
 XX Chimeric.
 XX Key Location/Qualifiers
 XX Misc-difference 1. 342
 XX /label= OTHER
 XX /note= "Xaa=unknown"
 XX WO200025722-A2.
 XX 11-MAY-2000.
 XX 21-OCT-1999; 99WO-SF001896.
 XX 02-NOV-1998; 98US-0106652P.
 XX 22-SEP-1999; 99US-00401636.
 XX (RESI-) RESISTENTIA PHARM AB.
 XX Hellman LT;
 XX WPI; 2000-365342/31.
 XX Immunogenic polypeptides useful for preventing the harmful effects of
 XX immunoglobulin E in mammals.
 XX Disclosure; Fig 2; 50pp; English.
 XX The present sequence is an immunogenic peptide consisting of the heavy
 XX chain constant regions 2 and 4 of the opossum IgE and the heavy chain
 XX constant region 3 created from a combination of the one from the rat and
 XX the one from the opossum. It was shown to cause a stronger polyclonal
 XX anti-self IgE response than peptides consisting of the same regions from
 XX one mammal. Immunogenic peptides, particularly those consisting of
 XX different heavy chain constant regions, can be used for vaccination in
 XX humans, against bacterial and viral infections and allergies, such as
 XX asthma, fur, pollen and food allergies and eczema. (Updated on 12-SEP-
 XX 2003 to standardise OS field)
 XX Sequence 342 AA;
 XX Query Match 74.1%; Score 1375; DB 3; Length 342;
 XX Best Local Similarity 76.6%; Pred. No. 6e-106;
 XX Matches 262; Conservative 23; Mismatches 55; Indels 2; Gaps 2;
 QY 1 EFHHHHHTLSLPESGPTVITPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW 60
 DB 1 EFHHHHHTLSLPESGPTVITPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW 60
 QY 61 LVDGQAEHLFPYTTTRPKREGGQTFSLQSEVNITQGWSSNTYTCHVKHNGSIFEDSSR 120

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Db 61 LVDDQAEHLFPYTRPKREGQCTSLQSEVHITQQWHSSTYCHVKXXGSIFFDSR 120
Qy 121 KADSNPRGVSAYLSRPSFDLFIKSPITICLVVDLAPSKGTNLTWSRAGCKPVNHS 180
Db 121 RUSDDPRGVITLYLPPSPDLYEHGTGPKLTCLVLDL-ESEEHIXVTWVXRPXIGXAR 179
Qy 181 RKEEKOR-NGTLTIVTSLPVGTRDWTIEGETYQCRVTHPLPALMRSTTKLPKRLAPEV 239
Db 180 SLVVKEXYHGTFTXTSHLPVETDDMTDGTGXTYXXLESPPMIVILPTI-SALPGKELAPXV 239
Qy 240 YMLPPSPETGTRIVTCLIRGYPSEISVQWLFNNEEDHTGHTTTPQKHGTDPGFF 299
Db 240 YMLPPSPETGTRIVTCLIRGYPSEISVQWLFNNEEDHTGHTTTPQKHGTDPGFF 299
Qy 300 LYSRMLVNSIWEKGNLVTCTRVVHEALPGSRILEKSLHYSAG 341
Db 300 LYSRMLVNSIWEKGNLVTCTRVVHEALPGSRILEKSLHYSAG 341

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RESULT 11

AAO19667
ID AAO19667 standard; protein; 320 AA.

XX AC AAO19667;

XX DT 28-MAR-2003 (first entry)

XX DE Human IgE heavy chain constant region CH2-CH3-CH4 portion.

XX KW Human; IgE; immunoglobulin E; immunotherapy; immune disease;
KW Pcepilone receptor; autoimmune disease; constant region; heavy chain;
KW antiasthmatic; antiallergic; antiinflammatory; dermatological;
KW antiarthritic; antirheumatic; antidiabetic; neuroprotective;
XX CH2-CH3-CH4 region.

XX OS Homo sapiens.

XX PN WO20028317-A2.

XX PD 07-NOV-2002.

XX PF 01-MAY-2002; 2002WO-US013527.

XX PR 01-MAY-2001; 2001US-00847208.

XX PR 24-OCT-2001; 2001US-00000439.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Saxon A, Zhang X, Zhu D;

XX PS WPI; 2003-103456/09.

XX PT New fusion molecules comprising polypeptide sequences that bind to IgG
XX PT inhibitory receptor and native IgE receptor, useful for treating IgE-
XX PT mediated hypersensitivity reactions, e.g. asthma or allergies, or
XX PT autoimmune diseases.

XX PS Claim 21; Fig 6; 116pp; English.

XX CC The present invention relates to a fusion molecule comprising a first
XX CC polypeptide sequence capable of specific binding to a native IgG
XX CC inhibitory receptor consisting of an immune receptor tyrosine-based
XX CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,
XX CC functionally connected to a second polypeptide sequence capable of
XX CC specific binding directly or indirectly to a native IgE receptor
XX CC (FcεR1). Also provided are nucleotide sequences encoding such a
XX CC fusion protein. The fusion molecules and compositions are useful for
XX CC treating an IgE-mediated biological response, preferably an IgE-mediated
XX CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic
XX CC dermatitis, severe food allergies, chronic urticaria, angioedema or
XX CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,
XX CC type-I diabetes mellitus, or multiple sclerosis, and for preventing of,

CC or symptoms resulting from, a type I hypersensitivity reaction in a
CC subject receiving immunotherapy. The present sequence is the human IgE
CC heavy chain constant region CH2-CH3-CH4 portion

XX SQ Sequence 320 AA;

Query Match 56.0%; Score 1038.5; DB 6; Length 320;
Best Local Similarity 62.4%; Pred. No. 5.7e-78;
Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;

Qy 22 PPTVKLFHSCDPRGDAHSTIQLCLVSGSPAKVHVTLVVDQEAENLFPYTRPKREG 81

Db 3 PPTVKILQSCDGGHFPPTIQLCLVSGYTPGTINITWLEDQGVMD--VDLSTASTQE 60

Qy 82 GQFSLQSEVNIITQGMSSNTYTCVHKHNGSIFEDSSRKCADSNPRGVSAYLSRSPFD 141

Db 61 GELASTQSELTLSQKHWLSDRTYTCQVYQGHFTFEDSTKCADSNPRGVSAYLSRSPFD 120

Qy 142 LFIKSPITICLVVDLAPSKGTNLTWSRAGCKPVNHSRKEKQNGTLTIVTSLPVGT 201

Db 121 LFIKSPITICLVVDLAPSKGTNLTWSRAGCKPVNHSRKEKQNGTLTIVTSLPVGT 180

Qy 202 RDWIEGETYQCRVTHPLPALMRSTTKLPKRLAPEVYMLPPSPETGT--TRTVTCLI 259

Db 181 RDWIEGETYQCRVTHPLPALMRSTTKSGPAADEVYAF-ATPEWPGSRDKRTLACLI 239

Qy 260 RGFYPSISVQWLFNNEEDHTGHTTTPQKHGTDPSPFLYSRMLVNSIWEKGNLVT 319

Db 240 QNFMPEDISVQWLFNNEEDHTGHTTTPQKHGTDPSPFLYSRMLVNSIWEKGNLVT 297

Qy 320 RVVHEALPGSRILEKSLHYSAG 341

Db 298 RAVHEAASPSQTVQRAVSNVPG 319

RESULT 12

AAU80286

ID AAU80286 standard; protein; 323 AA.

XX AC AAU80286;

XX DT 30-JUL-2002 (first entry)

XX DE Human IgE C2-C3-C4 domains for E.Coli expression.

XX KW IgE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;
XX KW antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;
XX KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
XX KW heavy chain C domain.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200220038-A2.

XX PD 14-MAR-2002.

XX PF 06-SEP-2001; 2001WO-DK000579.

XX PR 06-SEP-2000; 2000DK-00001326.

XX PR 15-SEP-2000; 2000US-0232831P.

XX PA (PHAR-) PHARMEXA AS.

XX PI Klysner S, Von Hoegen P, Voldborg B, Gautam A;

XX DR WPI; 2002-383033/41.

XX DR N-PSDB; ABK51134.

XX PT Inducing immune response against autologous immunoglobulin E in an
XX PT animal, by effecting simultaneous presentation of cytotoxic T lymphocyte
XX PT epitope an/or B-cell epitope derived from the immunoglobulin.

```

PS Disclosure; Page 112-113; 151pp; English.
XX
CC This invention relates to a novel method for inducing an immune response
CC against autologous immunoglobulin E (IgE) in an animal. The method
CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte
CC (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell
CC epitope (TH epitope) which is foreign to the animal, by antigen
CC presenting cells (APCs) of the animal's immune system. The epitopes of
CC the invention may be used as a vaccine against allergic diseases. The
CC method of the invention is useful for inducing an immune response against
CC autologous IgE in an animal. This method is useful in the prevention and
CC treatment of allergic diseases such as anaphylaxis, allergic rhinitis,
CC asthma and atopic dermatitis. The present sequence represents the human
CC IgE heavy chain C2-C3-C4 domains optimised for expression in an E. Coli
CC system, this sequence was used to create the epitopes of the invention
XX
SQ Sequence 323 AA;

Query Match 56.0%; Score 1038.5; DB 5; Length 323;
Best Local Similarity 62.4%; Pred. No. 5.8e-78;
Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;

QY 22 PPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTWLDGQAEALFPVYTRPKREG 81
DB 6 PPTVKILQSSCDGGHFPPTIQLCLVSGYTGTTINITWLDGQVMD--VDLSTASTTQE 63
QY 82 GQTFSLQSEVNIQTGQWMSNTYTCVHKNGSIFEDSSRKCADSNPRGVSAYLSRPSFD 141
DB 64 GELASTQSELTLSQKHLSDRTYTCQVYQGHTEFDSSTKKCADSNPRGVSAYLSRPSFD 123
QY 142 LFIKSPPTITCLVVDLAPSKGTVNLWTSRASKPVNHSRKEEKQNGTLTSTLPVGT 201
DB 124 LFIKSPPTITCLVVDLAPSKGTVNLWTSRASKPVNHSRKEEKQNGTLTSTLPVGT 183
QY 202 RDIWIEGTYQCRVTHPHLPALMRSTTKLPKRLAPEVYMLPSPSETGT--TRVTCL 259
DB 184 RDIWIEGTYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAF--ATPEWFGSRDKRTLA 242
QY 260 RGFYPSSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFLYSRMLVKNKSIWEKGNL 319
DB 243 QNFMPEDISVQWLNHEVQLPDARHSTTPQRKTGS--GFFVFSRLLEVTRAENEQKDEF 300
QY 320 RVVHEALPGSRITLESLSHSYAG 341
DB 301 RAVHEAASPQTQVRAVSNPG 322

RESULT 14
AAU80284
ID AAU80284 standard; protein; 323 AA.
XX
AC AAU80284;
XX
XX 30-JUL-2002 (first entry)
XX
XX Human IgE heavy chain C2-C3-C4 domains.
XX
XX IgE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;
XX antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;
XX heavy chain C domain.

PS Disclosure; Page 112-113; 151pp; English.
XX
CC This invention relates to a novel method for inducing an immune response
CC against autologous immunoglobulin E (IgE) in an animal. The method
CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte
CC (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell
CC epitope (TH epitope) which is foreign to the animal, by antigen
CC presenting cells (APCs) of the animal's immune system. The epitopes of
CC the invention may be used as a vaccine against allergic diseases. The
CC method of the invention is useful for inducing an immune response against
CC autologous IgE in an animal. This method is useful in the prevention and
CC treatment of allergic diseases such as anaphylaxis, allergic rhinitis,
CC asthma and atopic dermatitis. The present sequence represents the human
CC IgE heavy chain C2-C3-C4 domains optimised for expression in an E. Coli
CC system, this sequence was used to create the epitopes of the invention
XX
SQ Sequence 323 AA;

Query Match 56.0%; Score 1038.5; DB 5; Length 323;
Best Local Similarity 62.4%; Pred. No. 5.8e-78;
Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;

QY 22 PPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTWLDGQAEALFPVYTRPKREG 81
DB 6 PPTVKILQSSCDGGHFPPTIQLCLVSGYTGTTINITWLDGQVMD--VDLSTASTTQE 63
QY 82 GQTFSLQSEVNIQTGQWMSNTYTCVHKNGSIFEDSSRKCADSNPRGVSAYLSRPSFD 141
DB 64 GELASTQSELTLSQKHLSDRTYTCQVYQGHTEFDSSTKKCADSNPRGVSAYLSRPSFD 123
QY 142 LFIKSPPTITCLVVDLAPSKGTVNLWTSRASKPVNHSRKEEKQNGTLTSTLPVGT 201
DB 124 LFIKSPPTITCLVVDLAPSKGTVNLWTSRASKPVNHSRKEEKQNGTLTSTLPVGT 183
QY 202 RDIWIEGTYQCRVTHPHLPALMRSTTKLPKRLAPEVYMLPSPSETGT--TRVTCL 259
DB 184 RDIWIEGTYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAF--ATPEWFGSRDKRTLA 242
QY 260 RGFYPSSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFLYSRMLVKNKSIWEKGNL 319
DB 243 QNFMPEDISVQWLNHEVQLPDARHSTTPQRKTGS--GFFVFSRLLEVTRAENEQKDEF 300
QY 320 RVVHEALPGSRITLESLSHSYAG 341
DB 301 RAVHEAASPQTQVRAVSNPG 322

RESULT 13
AAU80285
ID AAU80285 standard; protein; 323 AA.
XX
AC AAU80285;
XX
XX 30-JUL-2002 (first entry)
XX
XX Human IgE C2-C3-C4 domains for mammalian expression.
XX
XX IgE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;
XX antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;
XX vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
XX heavy chain C domain.
XX
XX Homo sapiens.
XX OS Synthetic.
XX
XX WO200220038-A2.
XX
XX 14-MAR-2002.
XX
XX 06-SEP-2001; 2001WO-DK000579.
XX
XX 06-SEP-2000; 2000DK-00001326.

```


KW	vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
KW	heavy chain C domain.
XX	Homo sapiens.
OS	
XX	
PH	Key
FT	Location/Qualifiers
FT	8..103
FT	/note= "IgE heavy chain C2 domain"
FT	100..114
FT	/note= "Epitope including C2C3 linker"
FT	104..111
FT	/note= "Linker between domains C2 and C3"
FT	112..211
FT	/label= "IgE heavy chain C3 domain"
FT	139..145
FT	/note= "Epitope in BC loop"
FT	167..175
FT	/note= "Epitope in DE loop"
FT	196..206
FT	/note= "Epitope in FG loop"
FT	210..218
FT	/note= "Epitope including C3C4 linker"
FT	212..215
FT	/note= "Linker between domains C3 and C4"
FT	216..317
FT	/note= "IgE heavy chain C4 domain"
XX	
PN	WO200220038-A2.
XX	
PD	14-MAR-2002.
XX	
PF	06-SEP-2001; 2001WO-DX000579.
XX	
PR	06-SEP-2000; 2000DK-00001326.
PR	15-SEP-2000; 2000US-0232831P.
XX	
XX	(PHAR-) PHARMEXA AS.
PA	
PI	Klysner S, Von Hoegen P, Voldborg B, Gautam A;
PI	WPI; 2002-383033/41.
DR	
XX	
PT	Inducing immune response against autologous immunoglobulin E in an animal, by effecting simultaneous presentation of cytotoxic T lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin.
PT	
PS	Disclosure; Page 105-106; 151pp; English.
XX	
CC	This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E (IgE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell epitope (TH epitope) which is foreign to the animal, by antigen presenting cells (APCs) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal, which is useful for downregulating autologous IgE in the animal. This method is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic rhinitis, asthma and atopic dermatitis. The present sequence represents the human IgE heavy chain C2-C3-C4 domains used to create the epitopes of the invention
XX	
SQ	Sequence 323 AA;
	Query Match 56.0%; Score 1038.5; DB 5; Length 323;
	Best Local Similarity 62.4%; Pred. No. 5.8e-78;
	Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;
QY	22 BPVVKLFHSSCDPRGDAHSTIQLCLVSGFSFAKVTWLVLDGQAENLFPYTRPREG 81 : : : : : : 6 PPVTKILQSCDGGGHFPPITQLCLVSGYTEGTINITWLBDGYMD--VDLSTASTQEQ 63
Dd	

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XX SQ Sequence 324 AA;
Query Match 56.0%; Score 1038.5; DB 2; Length 324;
Best Local Similarity 62.4%; Pred. No. 5.8e-78;
Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;

QY 22 PPTVKLFHSGCDPRGDHSTIQLLCLVSGFSPAKVHVWLVLDGQAEMLFPYTTTRPKREG 81
Db 7 PPTVKILQSSCDGGHFPFTIQLLCLVSGYTRGTINITWLEDGQYMD--VDLSTASTTQE 64
QY 82 GQTFSLQSEVNIQGGWMSNTYVCHVKNGSIFEDSRKCADSNPRGVSAVLSRPSPPD 141
Db 65 GELASTQSELTSQKHWLSDRITYTCQTYQGHTEFEDSTKKCADSNPRGVSAVLSRPSPPD 124
QY 142 LFIRKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKORNGTLTITSLPVGT 201
Db 125 LFIRKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKORNGTLTITSLPVGT 184
QY 202 RDWIEGETYQCRVTHPLPRALMRSTKLPGKRLAPEVYMLPPSPPEETGT--TRTVCLII 259
Db 185 RDWIEGETYQCRVTHPLPRALMRSTKTSGPRAAPEVIYAF-ATPEWPGSRDKRTLACLI 243
QY 260 RGFYPSFISVQWLFNNEEDHTGHTTTRPKDGHGTDPSFELYSRMLVNSIWEKGNLYTC 319
Db 244 QNFMPEDISVQWJHNEVQLPDARHSTTPQPKTKGS--GPFVFSRLEVTAEWEQKDETC 301
QY 320 RVVHEALPGSRITLESILHSAG 341
Db 302 RAVHEAASPSQTVORAVSVNPG 323
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Search completed: November 14, 2004, 15:06:52
Job time : 81 secs

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OM protein - protein search, using sw model

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Title: US-09-401-636-8

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Scoring table: BLOSUM62

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Searched: 1569699 seqs, 353819137 residues

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Minimum DB seq length: 0

Maximum DB seq length: 342

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1856	100.0	342	9	US-09-401-636-8
2	1856	100.0	342	14	US-10-176-664-8
3	1856	100.0	342	15	US-10-176-664-8
4	1786	96.2	338	15	US-10-438-794-6
5	1786	96.2	338	15	US-10-453-915-6
6	1644.5	88.6	341	9	US-09-401-636-11
7	1644.5	88.6	341	14	US-10-176-664-11
8	1644.5	88.6	341	15	US-10-176-664-11
9	1587.5	85.5	341	9	US-09-401-636-3
10	1587.5	85.5	341	14	US-10-176-664-3
11	1587.5	85.5	341	15	US-10-176-664-3
12	1568.5	84.5	341	9	US-09-401-636-9
13	1568.5	84.5	341	14	US-10-176-664-9

14	1568.5	84.5	341	15	US-10-673-594-9	Sequence 9, Appli
15	1553.5	83.7	341	9	US-09-401-636-4	Sequence 4, Appli
16	1553.5	83.7	341	14	US-10-176-664-4	Sequence 4, Appli
17	1553.5	83.7	341	15	US-10-176-664-4	Sequence 4, Appli
18	1528.5	82.4	341	9	US-09-401-636-6	Sequence 6, Appli
19	1528.5	82.4	341	14	US-10-176-664-6	Sequence 6, Appli
20	1528.5	82.4	341	15	US-10-176-664-6	Sequence 6, Appli
21	1519	81.8	342	9	US-09-401-636-5	Sequence 5, Appli
22	1519	81.8	342	14	US-10-176-664-5	Sequence 5, Appli
23	1519	81.8	342	15	US-10-176-664-5	Sequence 5, Appli
24	1498.5	80.7	337	15	US-10-438-794-3	Sequence 3, Appli
25	1498.5	80.7	337	15	US-10-453-915-3	Sequence 3, Appli
26	1038.5	56.0	320	10	US-09-847-208-6	Sequence 6, Appli
27	1038.5	56.0	320	14	US-10-000-439-6	Sequence 6, Appli
28	1038.5	56.0	323	9	US-09-949-375A-2	Sequence 2, Appli
29	1038.5	56.0	323	9	US-09-949-375A-4	Sequence 2, Appli
30	1038.5	56.0	323	9	US-09-949-375A-6	Sequence 6, Appli
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32	1038.5	56.0	323	16	US-10-363-954A-4	Sequence 4, Appli
33	1038.5	56.0	323	16	US-10-363-954A-6	Sequence 6, Appli
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35	1038.5	56.0	331	14	US-10-176-664-1	Sequence 1, Appli
36	1038.5	56.0	331	14	US-10-207-655-329	Sequence 329, App
37	1038.5	56.0	331	15	US-10-673-594-1	Sequence 1, Appli
38	1036.5	55.8	330	9	US-09-949-375A-10	Sequence 10, Appli
39	1036.5	55.8	330	16	US-10-363-954A-10	Sequence 10, Appli
40	1034.5	55.7	336	9	US-09-949-375A-8	Sequence 8, Appli
41	1034.5	55.7	336	16	US-10-363-954A-8	Sequence 8, Appli
42	791.5	42.6	222	16	US-10-704-406-3	Sequence 3, Appli
43	778.5	41.9	222	9	US-09-809-746-2	Sequence 2, Appli
44	778.5	41.9	222	10	US-09-809-746-6	Sequence 6, Appli
45	778.5	41.9	222	16	US-10-704-406-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-401-636-8
; Sequence 8, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-8

Query Match 100.0%; Score 1856; DB 9; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.5e-139;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	EFHHHHHTLSLPESGPVTIIPVTVKLFHSSCDPRGDAHSTIQLLCVSGFSPAKVHTW	60
Db	1	EFHHHHHTLSLPESGPVTIIPVTVKLFHSSCDPRGDAHSTIQLLCVSGFSPAKVHTW	60
Qy	61	LVDQAEANLFPYTTTRPKREGGOTFSLQSEVNITQCGWMSNTYTCHVKHNGSIFEDSSR	120
Db	61	LVDQAEANLFPYTTTRPKREGGOTFSLQSEVNITQCGWMSNTYTCHVKHNGSIFEDSSR	120
Qy	121	KCADSNRGVSAYLSRSPDLIRKSPITTCIWDLAPSKGVNLTWSASCKPVNHS	180

Db 121 KCADSNPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLWTSRASGKPVNHST 180
QY 181 RKEEKORNGTLVTSTLPVGTDRDWIEGETYQCRVTHPHLPALMRSTTKLPKRLAPEVY 240
Db 181 RKEEKORNGTLVTSTLPVGTDRDWIEGETYQCRVTHPHLPALMRSTTKLPKRLAPEVY 240
QY 241 MLPSPSEETGTRTITVCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFPL 300
Db 241 MLPSPSEETGTRTITVCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFPL 300
QY 301 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRITLKSLSHYSAGN 342
Db 301 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRITLKSLSHYSAGN 342

RESULT 2

US-10-176-664-8
; Sequence 8, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-8

Query Match 100.0%; Score 1856; DB 14; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.5e-139;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60
Db 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60
QY 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNIQGWSSNTYCHVKHNGSIFEDSSR 120
Db 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNIQGWSSNTYCHVKHNGSIFEDSSR 120
QY 121 KCADSNPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLWTSRASGKPVNHST 180
Db 121 KCADSNPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLWTSRASGKPVNHST 180
QY 181 RKEEKORNGTLVTSTLPVGTDRDWIEGETYQCRVTHPHLPALMRSTTKLPKRLAPEVY 240
Db 181 RKEEKORNGTLVTSTLPVGTDRDWIEGETYQCRVTHPHLPALMRSTTKLPKRLAPEVY 240
QY 241 MLPSPSEETGTRTITVCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFPL 300
Db 241 MLPSPSEETGTRTITVCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFPL 300
QY 301 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRITLKSLSHYSAGN 342
Db 301 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRITLKSLSHYSAGN 342

RESULT 3

US-10-673-594-8
; Sequence 8, Application US/10673594
; Publication No. US20040076625A1
; GENERAL INFORMATION:

; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/673,594
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-673-594-8

Query Match 100.0%; Score 1856; DB 15; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.5e-139;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60
Db 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60
QY 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNIQGWSSNTYCHVKHNGSIFEDSSR 120
Db 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNIQGWSSNTYCHVKHNGSIFEDSSR 120
QY 121 KCADSNPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLWTSRASGKPVNHST 180
Db 121 KCADSNPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLWTSRASGKPVNHST 180
QY 181 RKEEKORNGTLVTSTLPVGTDRDWIEGETYQCRVTHPHLPALMRSTTKLPKRLAPEVY 240
Db 181 RKEEKORNGTLVTSTLPVGTDRDWIEGETYQCRVTHPHLPALMRSTTKLPKRLAPEVY 240
QY 241 MLPSPSEETGTRTITVCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFPL 300
Db 241 MLPSPSEETGTRTITVCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFPL 300
QY 301 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRITLKSLSHYSAGN 342
Db 301 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRITLKSLSHYSAGN 342

RESULT 4

US-10-438-794-6
; Sequence 6, Application US/10438794
; Publication No. US20040038395A1
; GENERAL INFORMATION:
; APPLICANT: LUNDGREN, Mats
; APPLICANT: FUENTES, Alexis
; APPLICANT: MAGNUSSON, Ann-Christin
; TITLE OF INVENTION: Chimeric Ige Polypeptides and Host Cells
; FILE REFERENCE: 10223-017001
; CURRENT APPLICATION NUMBER: US/10/438,794
; CURRENT FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/382,552
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide designated OSO
US-10-438-794-6

Query Match

96.2%; Score 1786; DB 15; Length 338;


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; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-11

Query Match      88.6%; Score 1644.5; DB 14; Length 341;
Best Local Similarity 88.0%; Pred. No. 1.1e-122;
Matches 301; Conservative 17; Mismatches 23; Indels 1; Gaps 1;

QY 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60
DB 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60

QY 61 LVDQQAENLFPYTTTRPKREGGQTFSLQSEVNITQQWSSNTYTCVHKNGSIPEDSSR 120
DB 61 LVDQQAENLFPYTTTRPKREGGQTFSLQSEVNITQQWSSNTYTCVHKNGSIPEDSSR 120

QY 121 KCADSNPRGVSAVLSRPSFDLPIRKSPITITCLVVDLAPSKGTVALTWSRASKGVNHS 180
DB 121 KCADSNPRGVSAVLSRPSFDLPIRKSPITITCLVVDLAPSKGTVALTWSRASKGVNHS 180

QY 121 KCSESDPRGVTSYLSPPSLDLVHKAPKITCLVVDLATMEG-MNLTWYRESKEPVNPGP 179
DB 121 KCSESDPRGVTSYLSPPSLDLVHKAPKITCLVVDLATMEG-MNLTWYRESKEPVNPGP 179

QY 181 RKEEKORNGTLTVSTLPGVTRDWIEGETYQCRVTHPHLPRALMRSTTKLPKRLAPEVY 240
DB 181 RKEEKORNGTLTVSTLPGVTRDWIEGETYQCRVTHPHLPRALMRSTTKLPKRLAPEVY 240

QY 180 LNKKDHFNCTITVTSTLPVNTNDWIEGETYQCRVTHPHLPRKDIVRSIAKLPKRLAPEVY 239
DB 180 LNKKDHFNCTITVTSTLPVNTNDWIEGETYQCRVTHPHLPRKDIVRSIAKLPKRLAPEVY 239

QY 241 MLPPSPETGTRTTCVCLIRGFYPSISVQWLFNNEEDHTGHHTTRPKQKHGTDPSFFL 300
DB 241 MLPPSPETGTRTTCVCLIRGFYPSISVQWLFNNEEDHTGHHTTRPKQKHGTDPSFFL 300

QY 301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
DB 301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 341

RESULT 9
US-09-401-636-3
; Sequence 3, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-3

Query Match      85.5%; Score 1587.5; DB 9; Length 341;
Best Local Similarity 85.4%; Pred. No. 3.8e-118;
Matches 292; Conservative 21; Mismatches 28; Indels 1; Gaps 1;

QY 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60
DB 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60

QY 61 LVDQQAENLFPYTTTRPKREGGQTFSLQSEVNITQQWSSNTYTCVHKNGSIPEDSSR 120
DB 61 LVDQQAENLFPYTTTRPKREGGQTFSLQSEVNITQQWSSNTYTCVHKNGSIPEDSSR 120

QY 121 KCADSNPRGVSAVLSRPSFDLPIRKSPITITCLVVDLAPSKGTVALTWSRASKGVNHS 180
DB 121 KCADSNPRGVSAVLSRPSFDLPIRKSPITITCLVVDLAPSKGTVALTWSRASKGVNHS 180

QY 181 RKEEKORNGTLTVSTLPGVTRDWIEGETYQCRVTHPHLPRALMRSTTKLPKRLAPEVY 240
DB 181 RKEEKORNGTLTVSTLPGVTRDWIEGETYQCRVTHPHLPRALMRSTTKLPKRLAPEVY 240

QY 180 LVWKEQYNGTFTVTSHLPVNTDDWIEGDTYTCLESPPMPVPLIRITISKAPKRLAPEVY 239
DB 180 LVWKEQYNGTFTVTSHLPVNTDDWIEGDTYTCLESPPMPVPLIRITISKAPKRLAPEVY 239

QY 241 MLPPSPETGTRTTCVCLIRGFYPSISVQWLFNNEEDHTGHHTTRPKQKHGTDPSFFL 300
DB 241 MLPPSPETGTRTTCVCLIRGFYPSISVQWLFNNEEDHTGHHTTRPKQKHGTDPSFFL 300

QY 301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
DB 301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 341

RESULT 10
US-10-176-664-3
; Sequence 3, Application US/10176664
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; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-3

Query Match      85.5%; Score 1587.5; DB 14; Length 341;
Best Local Similarity 85.4%; Pred. No. 3.8e-118;
Matches 292; Conservative 21; Mismatches 28; Indels 1; Gaps 1;

QY 1 EFHHHHHTLSLPESGVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTW 60
Db 1 EFHHHHHTLSLPESGVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTW 60
QY 61 LVDGQAEANLFPYTRPRKREGGQTFSLQSEVNITQGMSSNTYTCVHKNGSIFEDSSR 120
Db 61 LVDGQAEANLFPYTRPRKREGGQTFSLQSEVNITQGMSSNTYTCVHKNGSIFEDSSR 120
QY 121 KCADSNPRGVSAYLSRPSFDFIRKSPITITCLVVDLAPSKGTNLTWSRASKGPNVHST 180
Db 121 KCADSNPRGVSAYLSRPSFDFIRKSPITITCLVVDLAPSKGTNLTWSRASKGPNVHST 180
QY 121 KCSDTDPRGISAYILPPTQDLPVKVPTIGCLIVDLA-SAENVKVTWSRSGGPNVPS 179
Db 121 KCSDTDPRGISAYILPPTQDLPVKVPTIGCLIVDLA-SAENVKVTWSRSGGPNVPS 179
QY 181 RKEEKQKNGTLTSTLPVGTDRDWIEGETYQCRVTHPLRALMRSTTKLPGRKLAPEVY 240
Db 181 RKEEKQKNGTLTSTLPVGTDRDWIEGETYQCRVTHPLRALMRSTTKLPGRKLAPEVY 240
QY 180 LVVKEQYNGTFTVTSHLPVNTDMEGDTYTCRLESPPMVEPLIRTISKAPGRKLAPEVY 239
Db 180 LVVKEQYNGTFTVTSHLPVNTDMEGDTYTCRLESPPMVEPLIRTISKAPGRKLAPEVY 239
QY 241 MLPPSPPEETGTRTTCVCLIRGFYPSSEISVQWLFNNEEDHTGHTTTRPQKHGTDPSPFFL 300
Db 241 MLPPSPPEETGTRTTCVCLIRGFYPSSEISVQWLFNNEEDHTGHTTTRPQKHGTDPSPFFL 300
QY 301 YSRMLVNKSIWEKGNLVTCTVWHEALPGSRITLKSLSHYSAGN 341
Db 301 YSRMLVNKSIWEKGNLVTCTVWHEALPGSRITLKSLSHYSAGN 341

RESULT 11
US-10-673-594-3
; Sequence 3, Application US/10673594
; Publication No. US20040076625A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/673,594
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-673-594-3

Query Match      85.5%; Score 1587.5; DB 14; Length 341;
Best Local Similarity 85.4%; Pred. No. 3.8e-118;
Matches 292; Conservative 21; Mismatches 28; Indels 1; Gaps 1;

QY 1 EFHHHHHTLSLPESGVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTW 60
Db 1 EFHHHHHTLSLPESGVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTW 60
QY 61 LVDGQAEANLFPYTRPRKREGGQTFSLQSEVNITQGMSSNTYTCVHKNGSIFEDSSR 120
Db 61 LVDGQAEANLFPYTRPRKREGGQTFSLQSEVNITQGMSSNTYTCVHKNGSIFEDSSR 120
QY 121 KCADSNPRGVSAYLSRPSFDFIRKSPITITCLVVDLAPSKGTNLTWSRASKGPNVHST 180
Db 121 KCADSNPRGVSAYLSRPSFDFIRKSPITITCLVVDLAPSKGTNLTWSRASKGPNVHST 180
QY 121 KCSDTDPRGISAYILPPTQDLPVKVPTIGCLIVDLA-SAENVKVTWSRSGGPNVPS 179
Db 121 KCSDTDPRGISAYILPPTQDLPVKVPTIGCLIVDLA-SAENVKVTWSRSGGPNVPS 179
QY 181 RKEEKQKNGTLTSTLPVGTDRDWIEGETYQCRVTHPLRALMRSTTKLPGRKLAPEVY 240
Db 181 RKEEKQKNGTLTSTLPVGTDRDWIEGETYQCRVTHPLRALMRSTTKLPGRKLAPEVY 240
QY 180 LVVKEQYNGTFTVTSHLPVNTDMEGDTYTCRLESPPMVEPLIRTISKAPGRKLAPEVY 239
Db 180 LVVKEQYNGTFTVTSHLPVNTDMEGDTYTCRLESPPMVEPLIRTISKAPGRKLAPEVY 239
QY 241 MLPPSPPEETGTRTTCVCLIRGFYPSSEISVQWLFNNEEDHTGHTTTRPQKHGTDPSPFFL 300
Db 241 MLPPSPPEETGTRTTCVCLIRGFYPSSEISVQWLFNNEEDHTGHTTTRPQKHGTDPSPFFL 300
QY 301 YSRMLVNKSIWEKGNLVTCTVWHEALPGSRITLKSLSHYSAGN 341
Db 301 YSRMLVNKSIWEKGNLVTCTVWHEALPGSRITLKSLSHYSAGN 341

RESULT 12
US-09-401-636-9
; Sequence 9, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-9

Query Match      84.5%; Score 1568.5; DB 9; Length 341;
Best Local Similarity 83.3%; Pred. No. 1.2e-116;
Matches 285; Conservative 20; Mismatches 36; Indels 1; Gaps 1;

QY 1 EFHHHHHTLSLPESGVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTW 60
Db 1 EFHHHHHTLSLPESGVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTW 60
QY 61 LVDGQAEANLFPYTRPRKREGGQTFSLQSEVNITQGMSSNTYTCVHKNGSIFEDSSR 120
Db 61 LVDGQAEANLFPYTRPRKREGGQTFSLQSEVNITQGMSSNTYTCVHKNGSIFEDSSR 120
QY 121 KCADSNPRGVSAYLSRPSFDFIRKSPITITCLVVDLAPSKGTNLTWSRASKGPNVHST 180
Db 121 KCADSNPRGVSAYLSRPSFDFIRKSPITITCLVVDLAPSKGTNLTWSRASKGPNVHST 180
QY 121 KCSDDEPRGVITLIPSPDLVYENGTPKLTCLVLDL-ESEENITVTVWERKKSIGAS 179
Db 121 KCSDDEPRGVITLIPSPDLVYENGTPKLTCLVLDL-ESEENITVTVWERKKSIGAS 179
QY 181 RKEEKQKNGTLTSTLPVGTDRDWIEGETYQCRVTHPLRALMRSTTKLPGRKLAPEVY 240
Db 181 RKEEKQKNGTLTSTLPVGTDRDWIEGETYQCRVTHPLRALMRSTTKLPGRKLAPEVY 240
QY 180 QRSTKHNATTSITSLPVDKDWIEGEGYQCRVDHFPKPIVRSITKLPGRKLAPEVY 239
Db 180 QRSTKHNATTSITSLPVDKDWIEGEGYQCRVDHFPKPIVRSITKLPGRKLAPEVY 239
QY 241 MLPPSPPEETGTRTTCVCLIRGFYPSSEISVQWLFNNEEDHTGHTTTRPQKHGTDPSPFFL 300
Db 241 MLPPSPPEETGTRTTCVCLIRGFYPSSEISVQWLFNNEEDHTGHTTTRPQKHGTDPSPFFL 300
```

Db 240 MLPPSPPEETGTRTVTCLIRGFYPSSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFL 299
Qy 301 YSRMLVNSIWEKGNLVTCTRVVHEALPGSRITLKSLSHYSAGN 342
Db 300 YSRMLVNSIWEKGNLVTCTRVVHEALPGSRITLKSLSHYSAGN 341

RESULT 13

US-10-176-664-9
; Sequence 9, Application US/10176664
; Publication No.: US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-9

Query Match 84.5%; Score 1568.5; DB 14; Length 341;
Best Local Similarity 83.3%; Pred. No. 1.2e-116;
Matches 285; Conservative 20; Mismatches 36; Indels 1; Gaps 1;

Qy 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTW 60
Db 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTW 60
Qy 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNITQGWSSNTYTCVKHNGSIFEDSSR 120
Db 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNITQGWSSNTYTCVKHNGSIFEDSSR 120
Qy 121 KCADSNPRGVSAYLSRPSFDLFIKSPITITCLVVDLAPSKGTVALTWSRASKPVNHS 180
Db 121 RCDSDPRGVITYLIPSPDLIYENGTPKLTCLVLDL-ESEENITVTVRERKKSIGSAS 179
Qy 181 RKEEKORNGTLVTSTLPVGTDRWIEGETYQCRVTHPHLPRALMRSTTKLPKRLAPEVY 240
Db 180 QRSTKHNNATTSITSLPVDADKDWIEGEGYQCRVDHPFPKPIVRSITKLPKRLAPEVY 239
Qy 241 MLPPSPPEETGTRTVTCLIRGFYPSSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFL 300
Db 240 MLPPSPPEETGTRTVTCLIRGFYPSSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFL 299
Qy 301 YSRMLVNSIWEKGNLVTCTRVVHEALPGSRITLKSLSHYSAGN 342
Db 300 YSRMLVNSIWEKGNLVTCTRVVHEALPGSRITLKSLSHYSAGN 341

RESULT 14

US-10-673-594-9
; Sequence 9, Application US/10673594
; Publication No.: US20040076625A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/673,594
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22

; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-673-594-9

Query Match 84.5%; Score 1568.5; DB 15; Length 341;
Best Local Similarity 83.3%; Pred. No. 1.2e-116;
Matches 285; Conservative 20; Mismatches 36; Indels 1; Gaps 1;
Qy 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTW 60
Db 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTW 60
Qy 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNITQGWSSNTYTCVKHNGSIFEDSSR 120
Db 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNITQGWSSNTYTCVKHNGSIFEDSSR 120
Qy 121 KCADSNPRGVSAYLSRPSFDLFIKSPITITCLVVDLAPSKGTVALTWSRASKPVNHS 180
Db 121 RCDSDPRGVITYLIPSPDLIYENGTPKLTCLVLDL-ESEENITVTVRERKKSIGSAS 179
Qy 181 RKEEKORNGTLVTSTLPVGTDRWIEGETYQCRVTHPHLPRALMRSTTKLPKRLAPEVY 240
Db 180 QRSTKHNNATTSITSLPVDADKDWIEGEGYQCRVDHPFPKPIVRSITKLPKRLAPEVY 239
Qy 241 MLPPSPPEETGTRTVTCLIRGFYPSSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFL 300
Db 240 MLPPSPPEETGTRTVTCLIRGFYPSSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFL 299
Qy 301 YSRMLVNSIWEKGNLVTCTRVVHEALPGSRITLKSLSHYSAGN 342
Db 300 YSRMLVNSIWEKGNLVTCTRVVHEALPGSRITLKSLSHYSAGN 341

RESULT 15
US-09-401-636-4
; Sequence 4, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-4

Query Match 83.7%; Score 1553.5; DB 9; Length 341;
Best Local Similarity 82.7%; Pred. No. 1.9e-115;
Matches 283; Conservative 21; Mismatches 37; Indels 1; Gaps 1;
Qy 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTW 60
Db 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTW 60
Qy 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNITQGWSSNTYTCVKHNGSIFEDSSR 120

Db	61	LVDGQAEANLFPYTTTPKREGGQTSLQSEVNIQGWSSNTYTYCHVKHNGSI	120
QY	121	KCADSNPRGVSAYLGRPSFDLFIKSPITICLVVDLAPSKCTVNLTWSRASGKPVNHST	180
Db	121	RCSDDEPRGVITYLIPPSPLDLYENGTPKLTCLVLDL-ESEENITVTWVREKKSIGSAS	179
QY	181	RKEEKQORNGTLVTSTLPVGTDRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVY	240
Db	180	QRSTKHHHATTSTSLPVDKADWIEGEGYQCRVDHPFKPIVRSITKLPKRLAPEVY	239
QY	241	MLPPSPETGTTRVTCLIRGFYPSEISVQWLFNNEEDHTGHHTTRPKQKHGTDPSFFL	300
Db	240	MLPPSPETGTTRVTCLIRGFYPSEISVQWLFNNEEDHTGHHTTRPKQKHGTDPSFFL	299
QY	301	YSRMLVNXSIWEKGNLVTQVVEALPGSRTLEKSLHYSAGN	342
Db	300	YSRMLVNXSIWEKGNLVTQVVEALPGSRTLEKSLHYSAGN	341

Search completed: November 14, 2004, 15:12:43
Job time : 80 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 15:03:41 ; Search time 24 Seconds
(without alignments)
1371.089 Million cell updates/sec

Title: US-09-401-636-8

Perfect score: 1856
Sequence: 1 EFHHHHHTLSLPSGPVTI.....HEALFGRSLTKSLHYSAGN 342

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 177956

Minimum DB seq length: 0
Maximum DB seq length: 342

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

1: Pir1: *
2: Pir2: *
3: Pir3: *
4: Pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	486.5	26.2	326	1	G2HU	Ig gamma-2 chain C
2	476	25.6	327	1	G4HU	Ig gamma-4 chain C
3	473.5	25.5	328	2	I47161	Ig gamma-3 chain c
4	468	25.2	328	2	I47160	Ig gamma 2b chain
5	465	25.1	328	2	I47159	Ig gamma 2a chain
6	463.5	25.0	328	2	I47158	Ig gamma 1 chain c
7	454	24.5	330	1	GHU	Ig gamma-1 chain C
8	447	24.1	277	2	I47162	Ig gamma 4 chain c
9	443.5	23.9	322	2	PS0019	Ig gamma-2a chain
10	437.5	23.6	323	1	GHRB	Ig gamma chain C r
11	436.5	23.5	326	2	PS0017	Ig gamma-1 chain C
12	428	23.1	329	2	SC0847	Ig gamma-2c chain
13	424.5	22.9	329	1	G2GP	Ig gamma-2 chain C
14	421	22.7	335	1	G2MSAB	Ig gamma-2a chain
15	418	22.5	308	2	G30554	Ig heavy chain C r
16	415.5	22.4	324	1	G1MS	Ig gamma-1 chain C
17	413	22.3	327	2	S06611	Ig gamma-2 chain C
18	402.5	21.7	255	4	S31866	Ig gamma-1 chain C
19	401.5	21.6	289	1	G3HUWI	Ig gamma-3 heavy c
20	397	21.4	329	1	G3MSC	Ig gamma-3 chain C
21	395.5	21.3	330	1	G2MSA	Ig gamma-2a chain
22	386.5	20.8	234	2	PT0207	Ig gamma chain C r
23	384	20.7	333	2	PS0018	Ig gamma-2b chain
24	370.5	20.0	340	2	I56230	Ig alpha-2 chain -
25	369.5	19.9	340	2	B22360	Ig alpha-2 chain C
26	359.5	19.4	340	1	A2HU	Ig alpha-2 chain C
27	343.5	18.5	342	2	A45966	Ig alpha chain C r
28	318.5	17.2	342	2	I47175	Ig alpha chain C r
29	308	16.6	180	2	I46732	Ig gamma heavy cha

30 306.5 16.5 338 2 S09276
31 298 16.1 339 2 S09264
32 292 15.7 335 2 S09275
33 285 15.4 152 2 S14236
34 282 15.2 115 2 I68731
35 280 15.1 115 2 I68727
36 272 14.7 220 2 C22360
37 261.5 14.1 107 2 I68726
38 260 14.0 299 1 AHRB
39 257 13.8 218 2 A36040
40 253.5 13.7 107 2 I68730
41 246.5 13.3 249 2 S69340
42 242 13.0 228 2 S03050
43 236.5 12.7 244 2 S12328
44 219 11.8 111 2 S43148
45 213.5 11.5 227 2 PH1215

ALIGNMENTS

RESULT 1

G2HU

Ig gamma-2 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004

C:Accession: A93906; A92809; A90752; A93132; A02148

R:Ellison, J.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982

A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain co

A:Reference number: A93906; MUID:82197621; PMID:6804948

A:Accession: A93906

A:Molecule type: DNA

A:Residues: 1-326 <ELL>

A:Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:932759; PIDN:CAB58438.1;

A:Note: Lys-326 is probably removed posttranslationally

R:Wang, A.C.; Tung, E.; Fudenberg, H.H.

J. Immunol. 125, 1048-1054, 1980

A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and

A:Reference number: A92809; MUID:81007873; PMID:6774012

A:Contents: myeloma protein T11

A:Accession: A92809

A:Molecule type: Protein

A:Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>

A:Note: Trp-156 is at or near the complement-binding site

R:Conneil, G.E.; Parr, D.M.; Hofmann, T.

Can. J. Biochem. 57, 758-767, 1979

A:Title: The amino acid sequences of the three heavy chain constant region domains of a

A:Reference number: A90752; MUID:8001357; PMID:113060

A:Contents: myeloma protein Zie

A:Accession: A90752

A:Molecule type: Protein

A:Residues: 1-24,'E',26-57,'EV',60-85,132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198

A:Note: this sequence has since been revised

R:Hofmann, T.; Parr, D.M.

Mol. Immunol. 16, 923-925, 1979

A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin

A:Reference number: A93132; MUID:80114419; PMID:118920

A:Contents: Zie

A:Accession: A93132

A:Molecule type: Protein

A:Residues: 238-275 <HOF>

R:Hofmann, T.; Parr, D.M.

submitted to the Atlas, March 1980

A:Reference number: A94591

A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268

A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidat

ned

R:Milstein, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.

A:Reference number: A90253; MUID:72033500; PMID:4940472

A:Contents: annotation; myeloma protein Sa, disulfide bonds

R;Frangione, B.; Milstein, C.; Pink, J.R.L.
 Nature 221, 145-148, 1969
 A;Title: Structural studies of immunoglobulin G.
 A;Reference number: A93157; MUID:69064124; PMID:5782707
 A;Contents: annotation; Sa, disulfide bonds
 C;Genetics:
 A;Gene: GDB:IGHG2
 A;Cross-references: GDB:119338; OMIM:147110
 A;Map position: 14q32.33-14q32.33
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
 C;Superfamily: immunoglobulin C region; immunoglobulin homology <IM1>
 F;20-85/Domain: immunoglobulin homology <IM2>
 F;239-306/Domain: immunoglobulin homology <IM3>
 F;14/Disulfide bonds: interchain (to light chain) #status experimental
 F;27-83,140-200,246-304/Disulfide bonds: #status experimental
 F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
 F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 26.2%; Score 486.5; DB 1; Length 326;
 Best Local Similarity 36.2%; Pred. No. 6.7e-29;
 Matches 117; Conservative 57; Mismatches 120; Indels 29; Gaps 11;

QY 35 RGAHSTIQLCLVSGFSPAKVHTW----LVDQBAENLFYTTTRPKREGGQTFSLQSE 90
 DB 16 RSTSESTAALGCLVKDYFPEPTVSNWNSGALTSG---VHTFPAVL----QSSGLYSLSSV 68

QY 91 VNTIQGWSSNTYTCHVKH---NGSIFEDSRKCADSNP-----RGVSAYLSRSPF 140
 DB 69 VTPSSNF-GTQYTCNVDHKPSNTKVDKVEKCCVCPAPVAGPSVFLFPKPK 127

QY 141 D-LFIRKSPITICLVVDLAPSKGTNLTWSRAGKPVNHSTRKEEKQKNGTLTVTSTLPV 199
 DB 128 DTLWISRTPEVTCVVDVSHEDPEVQFNWYDGVVHNAKTPREEQFNSTFRVVSULTV 187

QY 200 GTRDWIEGTQYQCRVTHPLPALWSTTKLPGKRLAPEVYMLPPSPPE-TGTTTFTVCL 258
 DB 188 VHODWLNGKEYCKVSNKGLPAIEKTSIKGQPREPQVYTLPPSREMTKNQVSLTCL 247

QY 259 IRGFYSEISVQWLFNNEEDHTGHTTTPQKHGTDPSFFLYSRMLVNKSWKGNLVT 318
 DB 248 VKGFYSPDIWESNGQPEN--NYKTPPMLD--SDGSFFLYSKLTVDKSRWQGNVFS 303

QY 319 CRVWHEALPGSRTLEKSLHYSAG 341
 DB 304 CSVMHEALHNHYT-QKSLSLSPG 325

RESULT 2
 G4HU
 Ig gamma-4 chain C region - human
 C;Species: Homo sapiens (man)
 C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
 C;Accession: A90933; A90249; A02150
 R;Ellison, J.; Buxbaum, J.; Hood, L.
 DNA 1, 11-18, 1981
 A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
 A;Reference number: A90933; MUID:83157104; PMID:6299662
 A;Accession: A90933
 A;Molecule type: DNA
 A;Residues: 1-327 <ELL>
 A;Cross-references: UNIPROT:P01861
 A;Note: the sequence was determined from the germline gene
 R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
 Biochem. J. 117, 33-47, 1970
 A;Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant r
 A;Reference number: A90249; MUID:70207560; PMID:4192699
 A;Accession: A90249
 A;Molecule type: protein
 A;Residues: 1-30;81-326 <PIN>
 C;Genetics:

A;Gene: GDB:IGHG4
 A;Cross-references: GDB:119340; OMIM:147130
 A;Map position: 14q32.33-14q32.33
 A;Introns: 99/1; 111/1; 221/1
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F;20-85/Domain: immunoglobulin homology <IM1>
 F;99-110/Region: hinge
 F;134-203/Domain: immunoglobulin homology <IM2>
 F;240-307/Domain: immunoglobulin homology <IM3>
 F;14/Disulfide bonds: interchain (to light chain) #status experimental
 F;27-83,141-201,247-305/Disulfide bonds: #status predicted
 F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
 F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 25.6%; Score 476; DB 1; Length 327;
 Best Local Similarity 35.8%; Pred. No. 4.1e-28;
 Matches 116; Conservative 57; Mismatches 121; Indels 30; Gaps 10;

QY 35 RGAHSTIQLCLVSGFSPAKVHTW----LVDQBAENLFYTTTRPKREGGQTFSLQSE 90
 DB 16 RSTSESTAALGCLVKDYFPEPTVSNWNSGALTSG---VHTFPAVL----QSSGLYSLSSV 68

QY 91 VNTIQGWSSNTYTCHVKHNGSIFEDSRKCADSNP-----RGVSAYLSRSPF 139
 DB 69 VTPSSS-LGTQYTCNVDHKPSNTKVDKVEKSGYGPCCPAPFLGPGSVFLFPKPK 127

QY 140 FD-LFIRKSPITICLVVDLAPSKGTNLTWSRAGKPVNHSTRKEEKQKNGTLTVTSTLP 198
 DB 128 KDILMISRTPEVTCVVDVSDQEDPEVQFNWYDGVVHNAKTPREEQFNSTFRVVSULTV 187

QY 199 GTRDWIEGTQYQCRVTHPLPALWSTTKLPGKRLAPEVYMLPPSPPE-TGTTTFTVTC 257
 DB 188 VLHQDWLNGKEYCKVSNKGLPSIEKTSIKAKGQPREPQVYTLPPSREMTKNQVSLTC 247

QY 258 LRGFYSEISVQWLFNNEEDHTGHTTTPQKHGTDPSFFLYSRMLVNKSWKGNLIV 317
 DB 248 LVKGFYSPDIWESNGQPEN--NYKTPPVLID--SDGSFFLYSLTLVDKSRWQGNVFS 303

QY 318 CRVWHEALPGSRTLEKSLHYSAG 341
 DB 304 CSVMHEALHNHYT-QKSLSLSLG 326

RESULT 3
 147161
 Ig gamma 3 chain constant region - pig (fragment)
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
 C;Accession: 147161
 R;Kaczkovics, J.; Sun, J.; Butler, J.E.
 J. Immunol. 153, 3565-3573, 1994
 A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
 A;Reference number: 147158; MUID:95015845; PMID:7930579
 A;Accession: 147161
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-328 <KAC>
 A;Cross-references: EMBL:U03781; NID:G433127; PIDN:AAA52219.1; PID:G433128
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 F;133-202/Domain: immunoglobulin homology <IM>

Query Match 25.5%; Score 473.5; DB 2; Length 328;
 Best Local Similarity 33.7%; Pred. No. 6.3e-28;
 Matches 109; Conservative 59; Mismatches 128; Indels 27; Gaps 9;

QY 35 RGAHSTIQLCLVSGFSPAKVHTW----LVDQBAENLFYTTTRPKREGGQTFSLQSE 90
 DB 16 RDTSGPNVAGLCLASSYFPEPTVMTWNSGALTSG---VHTFSPVLQF---SGLYSLSSM 68

Qy	91	VNITQOMWSSNTYTCYVXKNGSIFEDSSRK-----CADSNPRGVSAYILSRPSPF	140
Db	69	VTVPASS-LSSXSXTCNVNHEATTTKVDKRVGTKTKPPCPCPGCEVAGSVFIFFPKK	127
Qy	141	D-LFRKSPITICLVVDLAPSGKGVNLTWSRASGKPVNHSTRKEEKORNGTLLVTSTLPP	199
Db	128	DTLMSIQTEPVTCVVVDVSKHAEVQPSWYVDGVEVHTAETRPKEQFNSTYRVVSVLP	187
Qy	200	GTRDMIEGETYOCRYTHEHLPRALMRSTKLPGKELAPEVYMLPPSPPEENGTR--TVTCL	258
Db	188	QHQQDWLKGKFKCKVNNVDLPAPITRTLSKAGQSRPEQVYTLPPPAEELSRSKVTVCL	247
Qy	259	IGFYPSEILSOWLFNNEEDTGHHTTTRPKDGHGTDPSFPLYSRMLVNKSIWEKNLVT	318
Db	248	VIGFYPPDDIHVEKNGQFPEGNYTRPTPOQD--VDGTFFLYSKLAVDKARWDHGETPE	305
Qy	319	CRWHEALPGSRTLKSLHYSAG	341
Db	306	CAMWHEALHNHYT-OKSISKTOG	327

RESULT 4
I47160
IG gamma 2b chain constant region - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C/Accession: I47160
R/Kacs Kovacs, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3585-3573, 1994
A/Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A/Reference number: I47158; NUID:95015845; PMID:7930579
A/Accession: I47160
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-328 <XAC>
A/Cross-references: EMBL:U03780; NID:G433125; PIDN:AAA52218.1; PID:G433125
C/Genetics:
A/Gene: IgG2b
C/Superfamily: immunoglobulin C region; immunoglobulin homology
P:133-202/Domain: immunoglobulin homology <TM>

Query Match	25.2%; Score 468; DB 2; Length 328;
Best Local Similarity	32.8%; Pred. No. 1.6e-27;
Matches	111; Conservative 61; Mismatches 136; Indels 30; Gaps 11;
Qy	22 PPIVKLPH--SSCDPRGDAHSTIOLLCLVSGFSFAKVHTW----LVDGQEAENLFPYTT 75
Db	2 PKTAPLYPTAPCG-RDTSGNVALGCLASSYFPEPVITWTNSGALTSG---VHTFBSVL 57
Qy	76 RPKEGGGOTSLQSEVINITQGMWSSNTYTCVHXKNGSI FEDSRK-----CADS 125
Db	58 QP-----SGLYSLSMVTVPASS-IUSSKSYICVNNHPATITTKVDKVGTKTKPPCFPCAP 112
Qy	126 NPGVSAYLGRPPFD-LFIRKSTITICLVVDLAPSKGTVNLTVWSRAGSKPVNHSRKEE 184
Db	113 ESPGFSVFIEPPKPKDTLMISRTQVTCVVVDVSDQENPEVQFSVYVDGVEVHTAQTRKE 172
Qy	185 KORNGTITVSTLIPVCHTRDMEGTGYOCRVTTHPLPALMRSTTKLPCKRLAPVWMLPP 244
Db	173 EQFNSTYRVSVSLPIQIQDMLNGKEFKCKVNNKDLPAITRIISAKAGQTRQPVYTLPP 232
Qy	245 SPESGTGTR-TVTCLIRGHFPESEISVOWLFNNEEDHTGHHTTTPQKHGDPDSFFLYSR 303
Db	233 HAELSRSKYSITCLVIGFPDIDVWQRNGQPEPEGNVYTTTPQQD--VDGTYFLYSK 290
Qy	304 MLVNKSWEKGNLTVCRVVHEALPGSRTLEKSLHYSAG 341
Db	291 FSDVKASWGGGIFOCAMWHEALHNHYT-OXSIKTI PG 327

RESULT 5
I47159

Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MCID:95015845; PMID:7930579
A:Accession: I47159
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03779; NID:G433123; PIDN:AAA52217.1; PID:G433124
C:Genetics:
A:Gene: I9G2a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMW>

Query Match	25.1%	Score 465;	DB 2;	Length 328;
Best Local Similarity	33.0%;	Pred. No. 2.7e-27;		
Matches	111;	Conservative 58;	Mismatches 137;	Indels 30; Gaps 10;
Qy	22	PPVTKLPHSSCDPRGDAHSIQLCLIVSGFSPAKVHVW----	LVDQGEAENLPFYTRP	77
Db	6	PSVYPLAPCGRDTSG----	PNVALGCLASSYFPPEVTVWNSGALSSG----	VHTFSPSVLQP 59
Qy	78	KREGGQFSLQSEVNITQGMWSNNTYTCVKGINGSIFEDSSRK----		CADSNP 127
Db	60	-----SGLYSLSSMWTVPASS--LSKSKYTCNVNHPATTTKYDKVGTKTGPPCPCIPACES		114
Qy	128	RGVSAYLSRSPFPD-LFIRKSPITTCVLVDLAPSKGTVNLTWRSASOKPVNHNSTRKBEEK		186
Db	115	PGPSVFIFPPKPKDTLMISRTPTQVCVVVDVSOENPEVQPSWYVDGVEVHTAQTARPKBEEQ		174
Qy	187	RNGTLTVTSITLPGVTRDWIETGEYQCYVTHPHLPALMRSTTKLPGKELAPEVVMLPSP		246
Db	175	FNSTYRVSVLPIQHQDMLNGKFKCKVNNKDLPAPIRIISKAGQTRBPQVVTLPHPA		234
Qy	247	EETGTTB-TWTCILIRGPYPSEISVQWLFNNBDEHTGHTTTRPOKDHGTPSPFELYSRML		305
Db	235	EELSRSKVSTICLVIGYPDPDIDVEWORNQCPPEGNYRTPTPOOD--VDGTLYFLSKFS		292
Qy	306	VNKSIMEKGNLTCRVVHEALPGSRITLXSLHYSAG		341
b	293	VDKASWGGGIFOCAYVHEALHNHYT-OKGISKTPG		327

```

RESULT 6
I47158
Ig gamma 1 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47158
J:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47158
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <YAC>
A:Cross-references: EMBL:U03778; NID:G433121; PIDN:AAAS2216.1; PID:G433122
C:Genetics:
A:Gene: IgG1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
P:133-202/Domain: immunoglobulin homology <IMM>

```

Query Match 25.0%; Score 463.5; DB 2; Length 328;
Best Local Similarity 33.9%; Pred.No. 3.5e-27;
Matches 107; Conservative 58; Mismatches 124; Indels 27; Gaps 9;
Qy 42 IQLICLVSGFSPAKVHTW---LVDQGEAENLPYTRPKREGQTFSLQSEVNIQTGQ 97

Db 23 VALGCLASSYFPPVPTVTWNSGALTSQ---VHTFSPVLQP-----SGLYSLSSMTVTPASS 75
 QY 98 WMSNTYTCVKNKNGSIFEDSRK-----CADSNPRGVSAVYLSRPSFD-LFTRK 146
 Db 76 -LSKKYTCNVNHPATTTTKVDRVGHQPTCPICFGCVAGPSVFIPPKPKOTLMISQ 134
 QY 147 SPRTICLVVDLAPSKGTVALTWSRASKPWNHSTRKEERQNGTLTSTLPGVRDWE 206
 Db 135 TPEVTCVVDVSKHAHVQFSWTVDGVEVHTAETRPKEQFNSTYRVSVLPIQHODMLK 194
 QY 207 GETYQCRVTHPLPRALMSTYKLPKRLAPEVYMLPPSPBTGTTR-TVTCLIRGFVPS 265
 Db 195 GKFKCKVNVNVDLPAPITRTISAIGQSRPQVYTLPPPAEELSRKSVTLTCLVIGFYPP 254
 QY 266 EISGVQLENNEEDHTGHTTTPQKHGTDPSFFLYSRMLVNSKIWEKGNLVTCRWHEA 325
 Db 255 DIHVWKNKGQPEPNTYRTTPQOD--VDGTFFLYSLAVDKARHGDKECAVMEHA 312
 QY 326 LPSGRTLEKSLHVSAG 341
 Db 313 LHHYTT-QKSISKTQ 327

RESULT 7

GHHU

Ig gamma-1 chain C region - human
 C/Species: Homo sapiens (man)
 C/Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004
 A/Accession: A93433; S33887; B90563; A90564; B91668; A91723; A02146
 R/Bilison, J.W.; Berson, B.J.; Hood, L.E.
 Nucleic Acids Res. 10, 4071-4079, 1982
 A/Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
 A/Reference number: A93433; NUID:82274238; PMID:6287432
 A/Accession: A93433
 A/Molecule type: DNA
 A/Residues: 1-330 <ELL>
 A/Cross-references: UNIPROT:P01857; EMBL:Z17370
 A/Note: this sequence has the Glm(17) allelic marker, 97-Lys, and the Glm(1) markers,
 A/Note: Lys-330 is removed after translation
 R/Harris, L.J.
 submitted to the EMBL Data Library, October 1992
 A/Reference number: S33904
 A/Accession: S36861
 A/Molecule type: DNA
 A/Residues: 2-330 <HAR>
 A/Cross-references: EMBL:Z17370
 R/Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
 Cell 29, 671-679, 1982
 A/Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
 A/Reference number: S33887; NUID:83001943; PMID:6811139
 A/Accession: S33987
 A/Molecule type: DNA
 A/Residues: 88-113;235-330 <TAK>
 A/Cross-references: EMBL:Z17370
 R/Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
 Biochemistry 9, 3161-3170, 1970
 A/Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
 A/Reference number: A90563; NUID:71064024; PMID:5489771
 A/Contents: myeloma protein Eu
 A/Accession: B90563
 A/Molecule type: protein
 A/Residues: 1-96,'R',98-135 <CUN>
 A/Note: this sequence has the Glm(3) marker, 97-Arg
 R/Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
 Biochemistry 9, 3171-3181, 1970
 A/Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen
 A/Reference number: A90564; NUID:71064025; PMID:5530842
 A/Contents: Eu
 A/Accession: A90564
 A/Molecule type: protein
 A/Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,
 A/Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met
 R/Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
 A/Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
 igen Primärstruktur.
 A/Reference number: A91668; NUID:77070269; PMID:826475
 A/Contents: myeloma protein Nie
 A/Accession: B91668
 A/Molecule type: protein
 A/Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
 A/Note: this sequence has the Glm(17) and Glm(1) markers
 R/Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
 A/Title: Die Primärstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOL
 A/Reference number: A91723; NUID:83289131; PMID:6884994
 A/Contents: myeloma protein KOL; disulfide bonds
 A/Accession: A91723
 A/Molecule type: protein
 A/Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
 A/Note: this sequence has the Glm(3) and Glm(non-1) markers
 R/Gall, W.E.; Edelman, G.M.
 Biochemistry 9, 3188-3196, 1970
 A/Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
 A/Reference number: A90565; NUID:71064027; PMID:4923144
 A/Contents: annotation; disulfide bonds
 R/Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
 A/Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
 enbromide cleavage products, and the disulfide bridges.
 A/Reference number: A91667; NUID:77070267; PMID:1002129
 A/Contents: annotation; disulfide bonds
 C/Genetics:
 A/Gene: GDB:IGHG1
 A/Cross-references: GDB:120085; OMIM:147100
 A/Map position: 14q32.33-14q32.33
 A/Introns: 99/1; 114/1; 224/1
 C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (Kap
 chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
 C/Superfamily: immunoglobulin C region; immunoglobulin homology
 C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F;137-206/Domain: immunoglobulin homology <IM1>
 F;243-310/Domain: immunoglobulin homology <IM2>
 F;27-83,144-204,250-308/Disulfide bonds: #status experimental
 F;103/Disulfide bonds: interchain (to light chain) #status experimental
 F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
 F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental
 Query Match 24.5%; Score 454; DB 1; Length 330;
 Best Local Similarity 34.4%; Pred. No. 1.8e-26;
 Matches 117; Conservative 57; Mismatches 130; Indels 36; Gaps 12;
 QY 22 PPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW---LVDGQEAENLFPVTRP 77
 Db 6 PSVFPLAPSSKSTSG---GTAALGCLVXYFPEPTVSNNSGALTSG---VHTFPAVL-- 57
 QY 78 KREGGQTFSLQSEVNITQGMSSNNTYCHVKNGSIFE-----DSRRKC----A 123
 Db 58 --QSSGLYSLSSVTVFSSS-LGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPCPA 114
 QY 124 DSNPRGVSAVLSRPSFD-LFTRKSPITCLVVDLAPSKGTVNLTWASRAGKPVNHSTK 182
 Db 115 PELLGGPSVFLFPKPKNDTLMISRTFVTCVVVDVSHEDPEVKFNWYDGVVHNKATXP 174
 QY 183 EEQRNGTLTSTLPGVTRDWTGEGTYQCRVTHPLPALMRSTTKLPKRLAPEVYML 242
 Db 175 REQYNSTYRVSVSLVVLHQDLNKGKCYKVSNNKALPAPIEKTSKAKGQPREPQVYTL 234
 QY 243 PPSPEE-TGTRVTVCLIRGFVPSISVQWLNFNNEEDHTGHTTTPQKHGTDSPFFLY 301
 Db 235 PPSRDELTKNQVSLTCLVKGFPSPDFAVEWESNGQEN--NYKTTFPVLD--SDGSFFLY 290
 QY 302 SRLMVKNSIWEKGNLVTCRWVHEALPGSRSTLEKSLHVSAG 341
 Db 291 SKLTVDKSRWQGNQNVFSCSWHEALHNHYT-QKSLSLSPG 329

RESULT 8
I47162
IG gamma 4 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47162
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IGH identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47162
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-277 <KAC>
A:Cross-references: EMBL:U03782; NID:G433129; PIDN:AAAS2220.1; PID:G433130
C:Genetics:
A:Superfamily: immunoglobulin C region; immunoglobulin homology
F:82-151/Domain: immunoglobulin homology <IMM>

Query Match 24.1%; Score 447; DB 2; Length 277;
Best Local Similarity 34.3%; Pred. No. 4.8e-26;
Matches 97; Conservative 57; Mismatches 109; Indels 20; Gaps 7;

QY 71 FVYTRPKREGGTFSLQSEVNITOGWSSNTYCHVXNGSIFEDSSRKCADSNP--- 127
DB 2 FSVLPQ-----SGLYLSNMVTPASS-ISSKSYTCNVNHPATTKVDRVGTTKPKPCP 56

QY 128 -----RGVSYLSRSPFD-LFTRKSPITCLVVDLAPSKGTNLTWSRAGKPVNHS 179
DB 57 ICPACGPGPSAIFPPKPKDILMSRTPKVTCTVVDVQENPEVQFVYVDGVVHTAQ 116

QY 180 TRKEEKORGLTVTSLPVGRDIEGETYOCRTVTHPLPRALMRSTKLGKGLAPV 239
DB 117 TRPKSEQFNSTRVSVLPIQDMLNGKEFKCKVNNKDLPAPIRIISKAGQTRBPQV 176

QY 240 YMLPPSPBEETGTR-TVTCLIRGFYSEISVQWLFNNEEDHTGHHTTRPQKHGTDRPSF 298
DB 177 YTLPPTEBLRSKVTCLTVGTFYPPDIDVEQWNGQPEPEGNRYTTPPQD--VDGTY 234

QY 299 FLYSRMLVNSIWEKGNLVTCRVHEALPGSRITLKSLSHSAG 341
DB 235 FLYSKLAVDKASQWQDGTFCQAVMHEALHNHT-QKSIFKTPG 276

RESULT 9
PS0019
IG gamma-2a chain C region - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C:Accession: PS0019; D25941
R:Brueggemann, M.
Gene 74, 473-482, 1988
A:Title: Evolution of the rat immunoglobulin gamma heavy-chain gene family.
A:Reference number: PS0017; MUID:89232738; PMID:3149946
A:Accession: PS0019
A:Molecule type: DNA
A:Residues: 1-322 <BRU>
A:Cross-references: UNIPROT:P20760
R:Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H.
Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
A:Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibody
A:Reference number: A25941; MUID:86287397; PMID:3016742
A:Accession: D25941
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 216-322 <BR2>
C:Genetics:
A:Introns: 98/1; 109/1; 216/1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin

F:20-84/Domain: immunoglobulin homology <IMM>

Query Match 23.9%; Score 443.5; DB 2; Length 322;
Best Local Similarity 34.4%; Pred. No. 1.1e-25;
Matches 110; Conservative 50; Mismatches 127; Indels 33; Gaps 12;

QY 38 AHSIQILLCLVSGSPAKVHTW---LVDQEAENLFPYTRPKREGGTFSLQSEVNI 93
DB 19 SNSVTLGCLVKGYFPEPVVTWNSGALSSG---VHTFPAVLQ-----SGLYITUTSVTV 70

QY 94 TOGQWSSNTYCHVXNGSIFEDSS---RKCADSNPRGV-----SAYLSRSPFD-L 142
DB 71 PSSTW-SSQAVTCNVAPASSTKYDKIVPREC---NPGCGTSGEVSSVFIFFPKTKDVL 126

QY 143 FIRKSPITCLVVDLAPSKGTNLTWSRAGKPVNHSRKEKQNRGLTVTSLPVGTR 202
DB 127 TITLTPKVTCTVVDISQNDPEVRFSWFIDDEVHTAQTAPKQSNSTLSVSELPVHR 186

QY 203 DWIEGETYOCRTVTHPLPRALMRSTKLGKGLAPVY-MLPPSPBEETGTRTTCCLIRG 261
DB 187 DWLNGTKFKVNSGAPPAPIEKSIKPEGTFRGPQVYTMAPPKEENTQSVSITCMVGK 246

QY 262 FYPSEISVQWLFNNEEDHTGHHTTRPQKHGTDRPSFFLYSRLVNSIWEKGNLVTCRV 321
DB 247 FYPDIYTEWKNQGPQE--NYKNTPTMD--TDGSYFLYSKLVNKVKTQCGNTFTCSV 302

QY 322 VHEALPGSRITLKSLSHSAG 341
DB 303 LHEGLHNHT-EKLSHSPG 321

RESULT 10

GHRB

IG gamma chain C region - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004

C:Accession: A91749; A90290; A93928; A90245; A94416; A02161

R:Bernstein, K.E.; Alexander, C.B.; Mage, R.G.

Immunogenetics 18, 387-397, 1983

A:Title: Nucleotide sequence of a rabbit IGH heavy chain from the recombinant F-I haplo

A:Reference number: A91749; MUID:84030930; PMID:6313520

A:Accession: A91749

A:Molecule type: mRNA

A:Residues: 1-323 <BER>

A:Cross-references: UNIPROT:P01870

A:Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Th

R:Pratt, D.M.; Mole, L.E.

Biochem. J. 151, 337-349, 1975

A:Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglo

A:Reference number: A90290; MUID:76135469; PMID:1243651

A:Accession: A90290

A:Molecule type: protein

A:Residues: 1-47, 'E', '49-71', 'PV', '72-128 <PRA>

R:Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.

Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982

A:Title: Heavy chain genes of rabbit IGH; isolation of a cDNA encoding gamma heavy chai

A:Reference number: A93928; MUID:83299917; PMID:6193512

A:Accession: A93928

A:Molecule type: mRNA

A:Residues: 88-103, 'M', '105-143, 'E', '145-184, 'A', '186, 'E', '188-266 <MAR>

A:Cross-references: GB:M16426; NID:G165111; PIDN:AAA31289.1; PID:G165112

A:Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic mark

R:Frutcher, R.O.; Jackson, S.A.; Mole, L.E.; Porter, R.R.

Biochem. J. 116, 249-259, 1970

A:Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin

A:Reference number: A90245; MUID:7010015; PMID:5461106

A:Accession: A90245

A:Molecule type: protein

A:Residues: 132-143, 'E', '145-161 <FRU>

R:Hall, R.L.; Lebovitz, R.E.; Fellows Jr., R.E.; Delaney, R.

in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell

A:Reference number: A94416

A:Accession: A94416

A:Molecule type: protein
A:Residues: 129-133;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q',
A>Note: This has the e15 allotypic marker, 185-Ala
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-92/Domain: immunoglobulin homology <IM1>
F;130-199/Domain: immunoglobulin homology <IM2>
F;236-303/Domain: immunoglobulin homology <IM3>
F;173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 23.6%; Score 437.5; DB 1; Length 323;
Best Local Similarity 34.3%; Pred. No. 2.9e-25;
Matches 113; Conservative 61; Mismatches 110; Indels 45; Gaps 14;

QY 36 GDA-HSTIOLLCVSGFSPAKVHVW-----LVDGQAEANLPPYTRPKREGQTFSLQSE 90
Db 16 GUTPSTVTLGLVKGYPVPTVWNSGTLTGVRT---FPSV----RQSSGLYSLSSV 68
QY 91 VNITQGMSSNTYTHCHVKH-----NGSIFEDSSRXCADSNPR---GVGAYLSRPPPF 140
Db 69 VSVTS-----SSQPVTCNVAPHTATKVTAPSTCSPTCPPELLGSPSVFPPAPK 124
QY 141 D-LFIRKSPITICLVVDLAPSKGTNLTW-----SRAGKPVNHSRKEKQKNGTLTV 193
Db 125 DTLMSRTPDEVTCVVVDVSDQDDPEVQFTWYINNEQVTRARPL-----REQQFNSTIRV 178
QY 194 TSTLPVGTDRWEGEYQCRVTHPLPALMRSTTKLPKRLAPEVY-MLPPSPRETTGT 252
Db 179 VSTLPITHQDMURGEFKCKVKNKALPAPIETIISKAGQPLEPKVYVWGPPELSRS 238
QY 253 RVTCLIRGFYSEISVQWLFNNEEDHTGHTTTRPKQDHGTPSPFLYSLRMLVNKS 312
Db 239 VSLTCMNGFYPSDISVEKNGKAE--DNYKTTTAVLD--SDGSYFLYNKLSVPTSEWQ 294
QY 313 KGNLTVCRVTHALPGSRLEKSLHYSAG 341
Db 295 RGDVFTCSVMHEALHNHT--QKSISRSPG 322

RESULT 11
PS0017
IG gamma-1 chain C region - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C:Accession: PS0017; C25941
R:Brueggemann, M.
Gene 74, 473-482, 1988
A:Title: Evolution of the rat immunoglobulin gamma heavy-chain gene family.
A:Reference number: PS0017; MUID:89232738; PMID:3149946
A:Accession: PS0017
A:Molecule type: DNA
A:Residues: 1-326 <BRU>
A:Cross-references: UNIPROT:P20759
R:Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H.
Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
A:Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibody
A:Reference number: A25941; MUID:86287397; PMID:3016742
A:Accession: C25941
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 220-326 <BR2>
C:Genetics:
A:Antons: 98/1; 113/1; 220/1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F;20-84/Domain: immunoglobulin homology <IMM>

Query Match 23.5%; Score 436.5; DB 2; Length 326;
Best Local Similarity 32.7%; Pred. No. 3.5e-25;
Matches 105; Conservative 54; Mismatches 131; Indels 31; Gaps 10;

QY 38 AHSTIOLLCVSGFSPAKVHVW-----LVDGQAEANLPPYTRPKREGQTFSLQSEVNI 93
Db 19 SNMWTLGLVKGYPPEPTVWNSGALSSG---VHTFPAVLQ-----SGLYTLSSVIV 70
QY 94 TQGMWSSNTYTHCHVKNRSIFE-----DSSRKCADSNPRGVSAYLSRSPFP- 141
Db 71 PSSTW-PSQVTCNVAPHTATKVTAPSTCSPTCPPELLGSPSVFPPAPKPDV 129
QY 142 LFIKSPITICLVVDLAPSKGTNLTWNSRAGKPVNHSRKEKQKNGTLTVTSTLPVGT 201
Db 130 LTTLTPKVTCTVVDISQDDPEVHFSWFDVDEVTATQTRPEEQFNSTFRSSELPIH 189
QY 202 RMIETGYQCRVTHPLPALMRSTTKLPKRLAPEVYMLPPSPBE-TGTRTTRVTLIR 260
Db 190 QDLNGRTFRCKVTSAAPSPIEKTIISKPEGRTOVPHVYTMSPPTKEMTQNEVSICTMKV 249
QY 261 GFYPSISVQWLFNNEEDHTGHTTTRPKQDHGTPSPFLYSLRMLVNKSIMWKGMLVTCR 320
Db 250 GFYPPDIYVWQNGQPOE--NYKNTPTTMD--TDSYFLSKLVNKKKQNGQNTFTCS 305
QY 321 VVHEALPGSRLEKSLHYSAG 341
Db 306 VLHEGLHNHT-EKSLSHSPG 325

RESULT 12
S00847
IG gamma-2c chain C region - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C:Accession: S00847
R:Brueggemann, M.; Delmaestro-Galfre, P.; Waldmann, H.; Calabi, F.
Eur. J. Immunol. 18, 317-319, 1988
A:Title: Sequence of a rat immunoglobulin gamma-2c heavy chain constant region cDNA: ext
A:Reference number: S00847; MUID:8816903; PMID:3127222
A:Accession: S00847
A:Molecule type: mRNA
A:Residues: 1-329 <BRU>
A:Cross-references: UNIPROT:P20762; EMBL:X07189; NID:957602; PIDN:CAA30169.1; PID:g66322
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F;20-84/Domain: immunoglobulin homology <IMM>

Query Match 23.1%; Score 428; DB 2; Length 329;
Best Local Similarity 32.4%; Pred. No. 1.5e-24;
Matches 110; Conservative 59; Mismatches 134; Indels 36; Gaps 13;

QY 23 PTYKLFHSSCDPRGDAHSTIOLLCVSGFSPAKVHVW-----LVDGQAEANLPPYTRPK 78
Db 6 PSVYPLVPGCS--GTSGSLVTLGLVKGYPPEPTVWNSGALSSG---VHTFPAVLQ-- 58
QY 79 REGQTFSLQSEVNIITQGMSSNTYTHCHVKH-----NGSIFEDSSRK-----CA-D 124
Db 59 ---SGLYTLSSSVTVPSSTW--SQVTCVVAHPATKSNLIKRIEPRRPRTDICSD 114
QY 125 SNPRGVSAYLSRSPFPD-LFIRKSPITICLVVDLAPSKGTNLTWNSRAGKPVNHSRKE 183
Db 115 DNLGRSPVRFPPKPKDILMITLTPKTCVVDVSEEPDQVQFSWFDVNVVFTAQTPH 174
QY 184 EKQNGTLTVSTLPVGTDRWEGEYQCRVTHPLPALMRSTTKLPKRLAPEVYMLP 243
Db 175 EQLNGTFRVYVTLTHIQHQMWSGKFKCKVKNKALPSPIEKTIISKPRKATPQVITIP 234
QY 244 PSPEETGTRT-TVTCLIRGFYSEISVQWLFNNEEDHTGHTTTRPKQDHGTPSPFLYS 302
Db 235 PPREQSKNKVSLTCVMTSPYPSISVEMERNGELSQ--DYKNTLPVLD--SDSEYFLYS 290
QY 303 RMLVNKSIMWKGMLVTCRVVHEALPGSRLEKSLHYSAG 341
Db 291 KLSVDYDSMWRGDIYTCVVVHEALHNHT--QRNLSRSPG 328

RESULT 13

G2GP

Ig gamma-2 chain C region - guinea pig
C:Species: Cavia porcellus (guinea pig)
C:Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 09-Jul-2004
C:Accession: A94553; A90352; A90359; A90384; A90385; A02151
R:Trischmann, T.M.
submitted to the Atlas, April 1975
A:Reference number: A94553
A:Accession: A94553
A:Molecule type: protein
A:Residues: 1-3 <TRI>
A:CROSS-references: UNIPROT:P01862
R:Birshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am
A:Reference number: A90352; MUID:71058471; PMID:5538606
A:Accession: A90352
A:Molecule type: protein
A:Residues: 4-68 <BIR>
R:Turner, K.J.; Cebra, J.J.
Biochemistry 10, 9-17, 1971
A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Am
A:Reference number: A90359; MUID:71058486; PMID:5538616
A:Accession: A90359
A:Molecule type: protein
A:Residues: 69-133;312-329 <TUR>
R:Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
A:Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.
A:Reference number: A90384; MUID:75036072; PMID:4429665
A:Accession: A90384
A:Molecule type: protein
A:Residues: 134-226 <TRA>
R:Trischmann, T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A:Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
A:Reference number: A90385; MUID:75036073; PMID:4609467
A:Accession: A90385
A:Molecule type: protein
A:Residues: 227-311 <TR2>
R:Oliveira, B.; Lamm, M.E.
Biochemistry 10, 26-31, 1971
A:Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
A:Reference number: A90354; MUID:71058474; PMID:4922544
A:Contents: annotation; disulfide bonds
A:Note: Cys-16 is involved in a heavy-light chain bond
A:Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
C:Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:21-81/Domain: immunoglobulin homology <IM1>
F:135-204/Domain: immunoglobulin homology <IM2>
F:241-310/Domain: immunoglobulin homology <IM3>
F:28-79/Disulfide bonds: #status experimental
F:142-202/Disulfide bonds: #status experimental
F:178/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:248-308/Disulfide bonds: #status experimental

Query Match 22.9%; Score 424.5; DB 1; Length 329;
Best Local Similarity 33.2%; Pred. No. 2.8e-24;
Matches 115; Conservative 52; Mismatches 136; Indels 43; Gaps 13;

QY 19 TIIPPTVKLFHSCDPRGDAHSTIQLCLVSGFSPAKVHTW----LVDGQEAENLFFYT 74
DB 4 TTAPSVFPLAASCVDTSQ---SNWTLGCLVKGFPFPTVKNSGALTSQ---VHTFFAV 57
QY 75 TPKREGGTFSLQSEVNTQGWSSNTYTCHVKHNGSIFEDSR----- 120
DB 58 LQ-----SGLSLTSMVTVP-----SSQKATCNVAHPASSTKVDXTVEIRTPZBPBCTC 107
QY 121 -KC-ADSNPRGSAVLSRSPFD-LFIRKSPITCLVLDLAPSKGTVNLTWASRGKPV- 176

DB 108 PKCPPENLGGSPVIFPPKPKDTLMISLTFRVTCVVVDVSDQDEVQFTWF-VDNKPVG 166
QY 177 NHTSKEKEKQKNGTITVTISTIPVGRDWEGETYQCRVTHPLPALMRSTTKLPKRLA 236
DB 167 NAEETPRVEQYNTTFRVESVLPIQHQDWLGRGKFKYKALPAPIEKTISKTKGAPRM 226
QY 237 PEVYMLPPSPBETGTR-TVTCILRGFYPSISVQWLFNNEEDHTGHHTTRPQKDHGTD 295
DB 227 PDVYTLPPSRDELSSKSVTCLINFFPADIHWNASNRVPVSEKYEKNTPTPED--AD 284
QY 296 PSFFLYSRMLVKNKSIWEKGNLVTRCVVHEALPGSRTEKSLHYSAG 341
DB 285 GSYFLYSLKTVDKSAWDQGTVTYTCVMHEALHNHVT-QKAISRSPG 329

RESULT 14
GZMSAB
Ig gamma-2a chain C region, secreted form (allele b) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C:Accession: A02153; A32656
R:Schreier, P.H.; Bothwell, A.L.M.; Mueller-Hilli, B.; Baltimore, D.
Proc. Natl. Acad. Sci. U.S.A. 78, 4495-4499, 1981
A:Title: Multiple differences between the nucleic acid sequences of the IgG2a(a) and Ig
A:Reference number: A02153; MUID:82037861; PMID:6170065
A:Accession: A02153
A:Molecule type: mRNA
A:Residues: 1-335 <SCH>
A:CROSS-references: UNIPROT:P01864; GB:J00479
A:Experimental source: strain C57BL/6
R:Dognin, M.J.; Lauwereys, M.; Strosberg, A.D.
Proc. Natl. Acad. Sci. U.S.A. 78, 4031-4035, 1981
A:Title: Multiple amino acid substitutions between murine gamma 2a heavy chain Fc regio
A:Reference number: A32656; MUID:82037777; PMID:6794027
A:Accession: A32656
A:Molecule type: protein
A:Residues: 118-267, 'E', 269-328, 'G', 330-334 <DOG>
C:Comment: Lys-335 is removed posttranslationally.
C:Complex: The sequence differs from that of the a allele, from BALB/c mice, at 15% of
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob
F:20-84/Domain: immunoglobulin homology <IM1>
F:98-118/Region: hinge
F:142-211/Domain: immunoglobulin homology <IM2>
F:248-315/Domain: immunoglobulin homology <IM3>
F:15/Disulfide bonds: interchain (to light chain) #status predicted
F:27-82,149-209,255-313/Disulfide bonds: #status predicted
F:108,117/Disulfide bonds: interchain (to heavy chain) #status predicted
F:185/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.7%; Score 421; DB 1; Length 335;
Best Local Similarity 31.7%; Pred. No. 5.2e-24;
Matches 106; Conservative 54; Mismatches 124; Indels 50; Gaps 9;

QY 36 GDAHSTIQLCLVSGFSPAKVHTW----LVDGQEAENLFPYTRPKREGGQTFSLQSEV 91
DB 17 GTTGSSTLGLVKGFPFPTVTWNSGSLSSGVH-----TFPALLOSGLYTLSSSV 68
QY 92 NITGQWSSNTYTCHVKHNGSIFEDSRKCADSNR----- 128
DB 69 TVTSNTW-PSQITCNVAHPAS---STKVDKIEFRVPITQPCPPHQRPVPCAAPDLL 123
QY 129 -GYSAYLSRSPFD-LFIRKSPITCLVLDLAPSKGTVNLTWASRGKPVNHSTRKEEK 186
DB 124 GGSVFIFPPKIKDVLMLISLSPMVTCTVDVSEDDPDVQISFWFNVEVHTAQOTHRED 193
QY 187 RNGTHLTVTPLVGRDWEGETYQCRVTHPLPALMRSTTKLPKRLAPEVYMLPPSP 246
DB 184 YNSTLRVVSALPIQHQDWKSGKFKCKVNNRPALEPSIEKTIKPRGPRVAPQVYVLP 243

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OM protein - protein search, using sw model

Run on: November 14, 2004, 15:03:40 ; Search time 97 Seconds
(without alignments)
2028.641 Million cell updates/sec

Title: US-09-401-636-8
Perfect score: 1856
Sequence: 1 EPHHHHTLSLPESGPVIT.....HEALPGSRLEKSLHVSAGN 342

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1224946

Minimum DB seq length: 0
Maximum DB seq length: 342

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	486.5	26.2	326	1 GC2_HUMAN	P01859 homo sapien
2	482.5	26.0	337	2 Q95M34	Q95M34 equus cabal
3	476	25.6	327	1 GC4_HUMAN	P01861 homo sapien
4	454	24.5	330	1 GC1_HUMAN	P01857 homo sapien
5	443.5	23.9	322	1 GCA_RAT	P20760 rattus norv
6	437.5	23.6	323	1 GC_RABIT	P01870 oryctolagus
7	436.5	23.5	326	1 GCI_RAT	P20759 rattus norv
8	428	23.1	329	1 GCC_RAT	P20762 rattus norv
9	424.5	22.9	329	1 GCX_CAVPO	P01862 cavia porce
10	421	22.7	335	1 GCAB_MOUSE	P01864 mus musculus
11	415.5	22.4	324	1 GC1_MOUSE	P01868 mus musculus
12	401.5	21.6	290	1 GC3_HUMAN	P01860 homo sapien
13	399.5	21.5	336	1 GCB_MOUSE	P01866 mus musculus
14	397	21.4	329	1 GC3_MOUSE	P22436 mus musculus
15	395.5	21.3	330	1 GCXA_MOUSE	P01863 mus musculus
16	384	20.7	333	1 GCB_RAT	P20761 rattus norv
17	369.5	19.9	340	1 ALC2_HUMAN	P01877 homo sapien
18	334.5	18.0	303	2 Q6KAM2	Q6KAM2 mus musculus
19	334.5	18.0	303	2 BAD21435	BAD21435 mus muscu
20	260	14.0	299	1 ALC_RABIT	P01879 oryctolagus
21	228	12.3	169	2 BAD00198	BAD00198 camelus d
22	224	12.1	190	2 BAD00199	BAD00199 camelus d
23	177.5	9.6	156	2 BAD00197	BAD00197 camelus d
24	176	9.5	234	2 AAh30813	AAh30813 homo sapi
25	173.5	9.3	240	2 BAC85234	BAC85234 homo sapi
26	173	9.3	236	2 Q6PIT5	Q6PIT5 homo sapien
27	173	9.3	236	2 Q6GMX9	Q6GMX9 homo sapien
28	173	9.3	236	2 AAh29444	AAh29444 homo sapi
29	167.5	9.0	268	2 Q90524	Q90524 ginglymosto
30	166.5	9.0	236	2 Q6PIH7	Q6PIH7 homo sapien
31	166.5	9.0	236	2 AAh34141	AAh34141 homo sapi

32	166.5	9.0	237	2 Q90545	Q90545 ginglymosto
33	165.5	8.9	267	2 Q90529	Q90529 ginglymosto
34	165	8.9	236	2 Q723Y4	Q723Y4 homo sapien
35	164	8.8	236	2 Q6GMX8	Q6GMX8 homo sapien
36	163	8.8	236	2 Q6GMX0	Q6GMX0 homo sapien
37	162.5	8.8	239	2 Q6P491	Q6P491 homo sapien
38	162.5	8.8	239	2 AAh63599	AAh63599 homo sapi
39	162	8.7	236	2 Q6GMW1	Q6GMW1 homo sapien
40	160.5	8.6	259	2 Q90530	Q90530 ginglymosto
41	160	8.6	234	2 Q72473	Q72473 homo sapien
42	159.5	8.6	235	2 BAC85358	BAC85358 homo sapi
43	159	8.6	234	2 Q6GMW3	Q6GMW3 homo sapien
44	158	8.5	103	1 LAC_CHICK	P00763 gallus gall
45	158	8.5	236	2 BAC85236	BAC85236 homo sapi

ALIGNMENTS

RESULT 1
GC2_HUMAN
ID GC2_HUMAN STANDARD; PRT; 326 AA.
AC P01859;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig gamma-2 chain C region.
GN Name=IGHG2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 2-326 FROM N.A.
RX MEDLINE=82197621; PubMed=8604948;
RA Ellison J.W., Hood L.E.;
RT "Linkage and sequence homology of two human immunoglobulin gamma heavy chain constant region genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
RN [2]
RP SEQUENCE OF 88-115 FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=83001943; PubMed=6811139;
RA Takahashi N., Ueda S., Obata M., Nakai S., Honjo T.;
RT "Structure of human immunoglobulin gamma genes: implications for evolution of a gene family.";
RL Cell 29:671-679(1982).
RN [3]
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=84235992; PubMed=6329676;
RA Krawinkel U., Rabbitts T.H.;
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass genes";
RL EMBO J. 1:403-407(1982).
RN [4]
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX MEDLINE=81007873; PubMed=6774012;
RA Wang A.-C., Tung E., Fudenberg H.H.;
RT "The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional implications.";
RL J. Immunol. 125:1048-1054(1980).
RN [5]
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX MEDLINE=80001357; PubMed=113060;
RA Connell G.E., Parr D.M., Hofmann T.;
RT "The amino acid sequences of the three heavy chain constant region domains of a human IgG2 myeloma protein.";
RL Can. J. Biochem. 57:759-767(1979).
RN [6]
RP SEQUENCE OF 238-275 (ZIE).
RX MEDLINE=80114419; PubMed=118920;

RA Hofmann T., Parr D.M.;
RT "A note of the amino acid sequence of residues 381-391 of human
RL immunoglobulin gamma chains.";
RL Mol. Immunol. 16:923-925(1979).
RN [7].
RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
RA Hofmann T., Parr D.M.;
RL Submitted (MAR-1980) to the PIR data bank.
RN [8].
RN SEQUENCE OF 1-121 (DOT).
RP MEDLINE=9535298; PubMed=7737130;
RA Scoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin monoclonal
RT immunoglobulins.";
RL Eur. J. Biochem. 228:886-893(1995).
RN [9].
RN DISULFIDE BONDS.
RP MEDLINE=72033500; PubMed=4940472;
RA Milstein C., Frangione B.;
RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
RL Biochem. J. 121:217-225(1971).
RN [10].
RN DISULFIDE BONDS.
RP MEDLINE=69064124; PubMed=5782707;
RA Frangione B., Milstein C., Pink J.R.L.;
RT "Structural studies of immunoglobulin G.";
RL Nature 221:145-148(1969).
CC -----
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CC -----
DR EMBL; J00230; AAB59393.1; -.
DR PIR; A93906; G2HU.
DR HSP; P01857; LOOX.
DR Genew; HGNC:5526; IGHG2.
DR MIM; 147110; -.
DR GO; 0005624; C-membrane fraction; NAS.
DR GO; 0003823; F-antigen binding; TAS.
DR GO; 0006955; P-immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Igcl; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON_TER 1 1
FT DOMAIN 1 98 CHI.
FT DOMAIN 99 110 Hinge.
FT DOMAIN 111 219 CHI.
FT DOMAIN 220 326 CHI.
FT DISULFID 14 14 Interchain (with a light chain).
FT DISULFID 27 83 Interchain (with a heavy chain).
FT DISULFID 102 102 Interchain (with a heavy chain).
FT DISULFID 103 103 Interchain (with a heavy chain).
FT DISULFID 106 106 Interchain (with a heavy chain).
FT DISULFID 109 109 Interchain (with a heavy chain).
FT DISULFID 140 200 Interchain (with a heavy chain).
FT DISULFID 246 304
FT SITE 156 156
FT VARIANT 60 60
AT OR NEAR THE COMPLEMENT-BINDING SITE.
S -> A (in mveloma proteins TIL and ZIE).
C -> S (in Ref. 3).
FT CONFLICT 109 109
FT SEQUENCE 326 AA; 35984 MW; 8310878C6878CF9C CRC64;
Query Match 26.2%; Score 486.5; DB 1; Length 326;

Best Local Similarity 36.2%; Pred. No. 2.4e-29;
Matches 117; Conservative 57; Mismatches 120; Indels 29; Gaps 11;

QY 35 RGDASTIQLCLVSGFSPAKVHTW-----LVDGQBAENLFFYTRPKREGGQTSLQSE 90
DB 16 RSTSESTAALGCLAVKDYFFPEPTVSNWNGALTSG---VHTFFAVL-----QSSGLYLSLV 68
QY 91 VNITQGMWSSNTYTCTCHVKH---NGSIFEDSSRKCADSNP-----RGVSAYLSRSPF 140
DB 69 VTFSSNF-GTQYTCNVDHKSNVTVDKVERKCCVECPCPAPPVAGPSVFLPPKPK 127
QY 141 D-LPIKSPITCLVVDLAPSKGTVNLWTSRAGSKPVNHSHTKKEKQKNGTILVSTLIV 199
DB 128 DTLMIKRTPEVTCVVDVSHEDDEVQFNMYVDGVVHNAKTPRESQFNTFRVWSVLT 187
QY 200 GTEDWIEGETYQCRVTHPLPRALMESTTKLPGKRLAPEVYMLPPSPPE-TGTRTVTCL 258
DB 188 VHQDWLNGKEYCKVKNKGLPAPFIEKTIISKQKQPREQVYTLPPSREEMTKNQVSLTCL 247
QY 259 IRGFYFSEISVQWLFNNEEDHTGHHTTTPQKHGTDPSFFLYSRMLVKNKSIWEKGNLVT 318
DB 248 VKGFYPSDIAVEWESNGQPEN--NYKTPPMLD--SDGSFFLYSKLTVDKSRMQQGVFS 303
QY 319 CRVTHEALPGSRTEKSLHYSAG 341
DB 304 CSMHEALHNHYT-QKSLSLSPG 325

RESULT 2
Q95M34 PRELIMINARY; PRT; 337 AA.
ID Q95M34
AC Q95M34;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Immunoglobulin gamma 1 heavy chain constant region (Fragment).
GN Name=IGHC1;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98383416; PubMed=9717671;
RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
RA Leibold W., Radbruch A.;
RT "Organization of the equine immunoglobulin heavy chain constant region
RT genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL Immunobiology 139:105-118(1998).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22172648; PubMed=12185539;
RA Wagner B., Greiser-Wilke I., Wege A.K., Radbruch A., Leibold W.;
RT "Evolution of the six horse IGHG genes and corresponding
RT immunoglobulin gamma heavy chains.";
RL Immunogenetics 54:353-364(2002).
DR EMBL; AJ300675; CAC44624.1; -.
DR HSP; P01857; 1H2H.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00407; Igcl; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
FT NON_TER 1 1
FT CHAIN <1 337 immunoglobulin gamma 1 heavy chain
FT constant region.
SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFDIF6 CRC64;

Query Match 26.0%; Score 482.5; DB 2; Length 337;
Best Local Similarity 32.8%; Pred. No. 5e-29;
Matches 113; Conservative 67; Mismatches 120; Indels 45; Gaps 12;

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QY 23 PTVKLFHSCDPRGDHSTIQLLCLVSGSPAKVHVW-----LVGQEAENLFPYTRPK 78
Db 6 PKVFALAPCGTISD--STVALGCLVSGYFPFVKVSMNSGLTSG---VHTFPSVL--- 57
QY 79 REGGQTFQSEVNITQGGWMSNTYCHVKNGSIFE-----DSSRKCADSN--P 127
Db 58 -QSSGFYSLSMVTVPASTW-TSEYICNVVHAASNFVKYDKIEIPDNHQKCDMSKCP 115
QY 128 R-----GVSAYLRSRPFDF-LFIRKSPITICLVVDLAPSKGTNLTWSRASKPVNH 178
Db 116 KCPAPELLGSPSVIFPPPKDMLTTRTEVTCVVVDVSDQBNPDVKFNWYMDGVEVRTA 175
QY 179 STRKEKQKNGTLTVSTLTPVGRDWIEGETYOCRVTHPLRALMRSTTKLPGKRLAPE 238
Db 176 TTRPKKEQNSYRVVSVLRIOHODWLSGKREKCKVNNQALPQPIERTITTKGSKBQ 235
QY 239 VYMLPSPBETGTR-TVTCLIRGFYSPISQWLFNNEEDTGHHTTRPKQDHTDPS 297
Db 236 VYVLAPHPDELKSKSVTCLVKDFYPPBEINIEWQSGOPELETKYSTITQAQD--SDGS 293
QY 298 FELYSRMLYNKSIWEKGNLVTCRVVHEALPGSRTEKSLHYSAGN 342
Db 294 YFLYSKLSVDNRNWOQGTTFTCGVWHEALHN-----HYTKRN 330

RESULT 3
GC4_HUMAN
ID GC4_HUMAN STANDARD; PRT; 327 AA.
AC P01861;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Ig gamma-4 chain C region.
GN Name=IGHG4;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83157104; PubMed=6299662;
RA Ellison J.W., Euxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18(1981).
RN [2]
RP SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192699;
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
RL Biochem. J. 117:33-47(1970).
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A90933; G4HU.
DR PDB; 1AQC; X-ray; A=118-323.
DR Genew; HGNC:5528; IGHG4.
DR MIM; 147130; -.
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; C:antigen binding; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003557; Ig.C1.
DR InterPro; IPR003006; Ig.MHC.
DR Pfam; PF00047; Ig; 3.
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DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW 3D-structure; Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON_TER 1 1 CH1.
FT DOMAIN 1 98 Hinge.
FT DOMAIN 99 110 Hinge.
FT DOMAIN 111 220 CH2.
FT DOMAIN 221 327 CH3.
FT DISULFID 14 14 Interchain (with a light chain).
FT DISULFID 27 83 Interchain (with a light chain).
FT DISULFID 106 106 Interchain (with a heavy chain).
FT DISULFID 109 109 Interchain (with a heavy chain).
FT DISULFID 141 201 Interchain (with a heavy chain).
FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;
Query Match 25.6%; Score 476; DB 1; Length 327;
Best Local Similarity 35.8%; Pred. No. 1.5e-28;
Matches 116; Conservative 57; Mismatches 121; Indels 30; Gaps 10;
QY 35 RGDHSTIQLLCLVSGSPAKVHVW-----LVGQEAENLFPYTRPKREGGQTFQSE 90
Db 16 RSTSESTAALGCLVKDYFPEFVTVSMNSGALTSG---VHTFPAVL-----QSSGLYSLSV 68
QY 91 VNITGGWMSNTYCHVKNGSIFEDSSRKCADSN-----RGVSAYLSRSPSP 139
Db 69 VTFPSSS-LGKTYTCNVVDHDKPSNTKVDKVESKYGPCPCPAPELGGSPVFLFPKP 127
QY 140 FD-LFIRKSPITICLVVDLAPSKGTNLTWSRASKPVNHSTKREKQKNGTLTVSTLP 198
Db 128 KDTLMISRTPEVTCVVVDVSDQBNPDVKFNWYMDGVEVHNAKTKPREQFNSTYRVSVLT 187
QY 199 VGFEDWIEGETYOCRVTHPLRALMRSTTKLPGKRLAPEVYMLPSPSEB-TGTRTVTC 257
Db 188 VLHODWLNKREYCKVSKNKGKLPSSIEKTSKAGQPREPQVYTLPPSQEETKNQVSLTC 247
QY 258 LIRGFYSPISQWLFNNEEDTGHHTTRPKQDHTDPSFFLYSRMLYNKSIWEKGNLV 317
Db 248 LVKGFYSPDIAVEWESNGQPN--NYKTTTPVLD--SDGSFFLYSRUTVDKSRWQEGNVF 303
QY 318 TCRVVEALPGSRTEKSLHYSAG 341
Db 304 SCVYHEALHNHYT-QKSLSLSG 326

RESULT 4
GC1_HUMAN
ID GC1_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Ig gamma-1 chain C region.
GN Name=IGHG1;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2]
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN BU).
EX MEDLINE=71064024; PubMed=5489771.
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
```

Biochemistry 9:3161-3170(1970).
 [3]
 SEQUENCE OF 136-329 (EU).
 MEDLINE=71064025; PubMed=5530842;
 Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
 Edelman G.M.;
 The covalent structure of a human gamma G-immunoglobulin. 8. Amino
 acid sequence of heavy-chain cyanoen bromide fragments Hs-H7.";
 Biochemistry 9:3171-3181(1970).
 [4]
 SEQUENCE (MYELOMA PROTEIN NIE).
 MEDLINE=77070269; PubMed=826475;
 Ponstingl H., Hilschmann N.;
 The rule of antibody structure. The primary structure of a monoclonal
 IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic
 peptides of the H-chain, alignment of the tryptic peptides and
 discussion of the complete structure.";
 Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
 [5]
 SEQUENCE (MYELOMA PROTEIN KOL). AND DISULFIDE BONDS.
 MEDLINE=83289131; PubMed=688494;
 Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
 Three-dimensional structure determination of antibodies. Primary
 structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
 Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
 [6]
 DISULFIDE BONDS.
 MEDLINE=71064027; PubMed=4923144;
 Gall W.E., Edelman G.M.;
 The covalent structure of a human gamma G-immunoglobulin. X.
 Intrachain disulfide bonds.";
 Biochemistry 9:3188-3196(1970).
 [7]
 DISULFIDE BONDS.
 MEDLINE=77070287; PubMed=1002129;
 Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 Rule of antibody structure. The primary structure of a monoclonal
 IgG1 immunoglobulin (myeloma protein NIE). I: purification and
 characterization of the protein, the L- and H-chains, the cyanogen
 bromide cleavage products, and the disulfide bridges.";
 Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 [8]
 X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 MEDLINE=81208100; PubMed=7236608;
 Deisenhofer J.;
 Crystallographic refinement and atomic models of a human Fc fragment
 and its complex with fragment B of protein A from *Staphylococcus*
 aureus at 2.9- and 2.8-A resolution.";
 Biochemistry 20:2361-2370(1981).
 CC -I- MISCELLANEOUS: NIE has the GIM(17) allotypic marker, 97-K, and the
 GIM(1) markers, 239-D and 241-L. KOL and EU sequences have the
 GIM(3) marker and the GIM (non-1) markers.
 CC -I- MISCELLANEOUS: NIE also differs in the amidation states of 35,
 116, 198, 269 and 272.
 CC -I- MISCELLANEOUS: EU also differs in the amidation states of residues
 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
 268-272.
 CC -I- MISCELLANEOUS: KOL also differs in the amidation states of
 residues 198, 267 and 272.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: J00228; AAC82527.1; ALT_INIT.
 DR PIR: A93433; GHU.
 DR PDB: 1A07; X-ray; H=1-103.
 DR PDB: 1D55; X-ray; B/H=1-101.
 DR PDB: 1D51; X-ray; H=1-101.

PDB: 1D6V; X-ray; H=1-101.
 PDB: 1DN2; X-ray; A/B=120-326.
 PDB: 1E4K; X-ray; A/B=106-329.
 PDB: 1FC1; X-ray; A/B=106-329.
 PDB: 1FC2; X-ray; D=106-329.
 PDB: 1FCC; X-ray; A=121-326.
 PDB: 1HZH; X-ray; H/K=1-330.
 PDB: 1I7Z; X-ray; B/D=1-103.
 PDB: 1IIX; X-ray; A/B=107-330.
 PDB: 1L6X; X-ray; A=120-326.
 PDB: 1OQX; X-ray; A/B=119-330.
 PDB: 2RCS; X-ray; H=1-103.
 Genew; HGNC:5525; IGHG1.
 DR GO: 0005624; C-membrane fraction; NAS.
 DR GO: 0003823; Frantigen binding; NAS.
 DR GO: 0006955; P-immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 Pfam: PF00047; Ig; 3.
 PROSITE: PS50835; IG_LIKE; 3.
 PROSITE: PS00290; IG_MHC; 2.
 3D-structure; Direct protein sequencing; Glycoprotein;
 Immunoglobulin C region; Immunoglobulin domain.
 FT NON TER 1 98
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 Hinge.
 FT DOMAIN 111 223 CH2.
 FT DOMAIN 224 330 CH3.
 FT DISULFID 27 83 Interchain (with light chain).
 FT DISULFID 103 103 Interchain (with heavy chain).
 FT DISULFID 112 112 Interchain (with heavy chain).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT CARBOHYD 180 180
 FT VARIANT 97 97
 FT VARIANT 239 239 N-linked (GlcNAc, ...)
 FT VARIANT 241 241 K -> R (in GIM(3) marker).
 FT STRAND 23 24 /FTID=VAR_003886.
 FT STRAND 26 33 D -> E (in GIM(non-1) marker).
 FT STRAND 38 38 /FTID=VAR_003887.
 FT STRAND 41 41 L -> M (in GIM(non-1) marker).
 FT TURN 42 45
 FT TURN 48 49
 FT TURN 50 52
 FT STRAND 57 58
 FT TURN 59 61
 FT STRAND 62 71
 FT STRAND 73 75
 FT HELIX 76 78
 FT TURN 82 87
 FT TURN 88 91
 FT STRAND 92 97
 FT TURN 102 103
 FT STRAND 122 126
 FT STRAND 130 134
 FT TURN 136 137
 FT STRAND 141 149
 FT STRAND 157 162
 FT TURN 163 164
 FT STRAND 165 167
 FT STRAND 171 172
 FT STRAND 176 177
 FT TURN 179 180
 FT STRAND 183 190
 FT STRAND 193 197
 FT TURN 198 199
 FT STRAND 202 207

FT TURN 209 210
 FT STRAND 215 219
 FT STRAND 227 227
 FT STRAND 230 234
 FT HELIX 238 242
 FT STRAND 245 256
 FT STRAND 261 266
 FT TURN 267 268
 FT STRAND 269 270
 FT STRAND 274 276
 FT STRAND 280 281
 FT TURN 283 284
 FT STRAND 287 296
 FT HELIX 297 301
 FT TURN 302 303
 FT STRAND 306 311
 FT TURN 313 314
 FT HELIX 316 318
 FT STRAND 319 324
 SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;

Query Match 24.5%; Score 454; DB 1; Length 330;
 Best Local Similarity 34.4%; Pred. No. 7.7e-27;
 Matches 117; Conservative 57; Mismatches 130; Indels 36; Gaps 12;

QY 22 PPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTV---LVDGQEAENLFPVYTRP 77
 Db 6 PSVFLAPSKSTSG---GTAALGCLVXDYFPEPTVSWNSGALTSG---VHTFPAVL-- 57

QY 78 KREGGOTFLOSHVNTQOWMSSNTYCHVKHNGSIFE-----DSRKC-----A 123
 Db 58 --QSSGLYSLSSVTVFPSS--LTQTYICNVNHPKSTNTKVDKVPKSCDKTHTCPPCPA 114

QY 124 DSNPRGVSVYLSRSPFD-LFTRKSPITICLVVDLAPSKGTNLWTSRASKPKVNHSTRK 182
 Db 115 PELLGSPSVFLPFPKPDITLMSRTPEVICVVDVSHEDPEVKFNWYDGVNNAKTRP 174

QY 183 EKQRNGTITVSTLPVGRDMEGETYQCRVTHPLPALMRSTTKLPKGLAPAEVYML 242
 Db 175 RBEQYNSTYVSVLVTLVHQDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREQVYTL 234

QY 243 RPSPEP-TGTRVTVCLIRGVPSETSVQWLFNNEEDHTGHTTTRPKQDHGTDSFFLY 301
 Db 235 PSRDELTKNQVSLTCLVKGFPYSDIAVEWENGPEN--NYKTTTPVLVD--SDGSFFLY 290

QY 302 SRLVYKSIWEKGNLVTCTRVVHEALPGSRITLKSLSHYSAG 341
 Db 291 SKLTVDKSRWQGNVFCSCWHEALHNHYT-QKSLSLSPG 329

RESULT 5
 GCA_RAT STANDARD; PRT; 322 AA.
 AC P20760;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Ig gamma-2A chain C region.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89232738; PubMed=3149946;
 RA Brueggemann M.;
 RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
 RL Gene 74:473-482(1988).
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
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 CC -----
 DR EMBL; M13804; AAA41376.1; ALT_INIT.
 DR PIR; PS0019; PS0019.
 DR PDB; 111A; X-ray; C=98-321, D=98-322.
 DR PDB; 111C; X-ray; A/B=98-322.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG cl.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00407; IGC1; 2.
 DR PROSITE; PS50835; IG LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW 3D-structure; Immunoglobulin C region; Immunoglobulin domain; Repeat.
 FT NON_TER 1
 FT DOMAIN 6 98 Ig-like 1.
 FT DOMAIN 115 212 Ig-like 2.
 FT DOMAIN 221 317 Ig-like 3.
 FT DISULFID 27 82 Interchain (with a heavy chain).
 FT DISULFID 102 102 Interchain (with a heavy chain).
 FT DISULFID 105 105 Interchain (with a heavy chain).
 FT DISULFID 107 107 Interchain (with a heavy chain).
 FT DISULFID 136 196
 FT DISULFID 242 300
 FT CARBOHYD 172 172
 SQ SEQUENCE 322 AA; 35186 MW; E8EA136A9DE01EDB CRC64;

Query Match 23.9%; Score 443.5; DB 1; Length 322;
 Best Local Similarity 34.4%; Pred. No. 4.8e-26;
 Matches 110; Conservative 50; Mismatches 127; Indels 33; Gaps 12;

QY 38 AHSTIQLCLVSGFSPAKVHVTV---LVDGQEAENLFPVYTRPKREGGOTFSLQSEVNI 93
 Db 19 SNSVTVLCLVKGFPPEPTVTVNSGALTSG---VHTFPAVLQ-----SGLYTLTSSVT 70

QY 94 TQGWMSNTVTVCHVKHNGSIFEDES---RKCADSNPRGV-----SAYLSRSPFD-L 142
 Db 71 PSSW--SSQAVTCNVAPASSTKVDKIVPREC---NPCGCTSEVSSVIFPPKTKDVL 126

QY 143 FIRKSPITICLVLDAPSKGTNLWTSRASKPKVNHSTRKEKQNGTTLVSTLPVGT 202
 Db 127 TITLTPKVTICVVDISQNDPEVRFSDVDVEVHTAQTHAPEKQSNSTLSVSELPVHR 186

QY 203 DWIEGETYQCRVTHPLPALMRSTTKLPKGLAPAEVY-MLPSPETGTTRVTVCLIRG 261
 Db 187 DWLNGKTFCKKVASGAPPAPIEKSISKEPGRGPQVYTWAPPEENTQSQVSIITCMVG 246

QY 262 FYPSEISVQWLFNNEEDHTGHTTTRPKQDHGTDPGFFLYSRMLVKNKSIWEKGNLVTCTRV 321
 Db 247 FYPEDIVTEKMGQPOE--NYKNTPTMD--TDGSVFLYKLVNKKETWQGNFTCSV 302

QY 322 VHEALPGSRITLKSLSHYSAG 341
 Db 303 LHEGLHNHHT-EKSLSHSPG 321

RESULT 6
 GCA_RAT STANDARD; PRT; 323 AA.
 AC P01870;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig gamma chain C region.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.

RA MEDLINE=84030930; PubMed=6313520; Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
F-1 haplotype.";
RL Immunogenetics 18:387-397(1983).
RN [2]
RP SEQUENCE OF 1-128.
RX MEDLINE=76135469; PubMed=1243651; Pratt D.M., Mole L.E.;
RA "Sequence studies on the constant region of the Fd sections of rabbit
immunoglobulin G of different allotype.";
RL Biochem. J. 151:337-349(1975).
RN [3]
RP SEQUENCE OF 88-266 FROM N.A.
RX MEDLINE=8329917; PubMed=6193512; Wartens C.L., Moore K.W., Steimer M., Hood L., Knight K.L.;
RA "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
heavy chain and identification of two genomic C gamma genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN [4]
RP SEQUENCE OF 132-161.
RX MEDLINE=70110015; PubMed=5461106; Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RA "Sequence studies of the Fd section of the heavy chain of rabbit
immunoglobulin G.";
RL Biochem. J. 116:249-259(1970).
RN [5]
RP SEQUENCE OF 129-131 AND 155-322.
RX Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
RA (In) Killander J. (eds.);
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
Stockholm (1967).
CC -1- MISCELLANEOUS: Ref.1 sequence has the D12 allotypic marker, 104-
Thr, and the E14 marker, 185-Thr. Ref.3 has the D11 and E15
markers and Ref.5 the E15 marker.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC -----
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CC -----
DR ENBL; M16426; AAA31289.1; -;
DR PIR; A91749; GHRB.
DR HSSP; P01852; INFN.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
DR Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain; Repeat.
FT NON_TER 1
FT DOMAIN 6 96 Ig-like 1.
FT DOMAIN 114 213 Ig-like 2.
FT DOMAIN 222 318 Ig-like 3.
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 N -> E (in Ref. 2).
FT CONFLICT 71 71 V -> VPV (in Ref. 2).
FT CONFLICT 144 144 Q -> E (in Ref. 3 and 4).
FT CONFLICT 173 173 N -> D (in Ref. 5).
FT CONFLICT 187 187 Q -> E (in Ref. 3 and 5).
FT CONFLICT 201 201 N -> D (in Ref. 5).
FT CONFLICT 218 218 Q -> E (in Ref. 5).
FT CONFLICT 233 233 E -> Q (in Ref. 5).
FT CONFLICT 246 246 N -> D (in Ref. 5).
FT CONFLICT 256 256 E -> G (in Ref. 5).
FT CONFLICT 256 256

FT CONFLICT 260 260 N -> D (in Ref. 5).
FT CONFLICT 266 266 N -> D (in Ref. 5).
FT CONFLICT 280 280 Y -> W (in Ref. 5).
FT CONFLICT 284 284 N -> S (in Ref. 5).
SQ SEQUENCE 323 AA; 35404 MW; 69B8AA118D579A8B CRC64;

Query Match 23.6%; Score 437.5; DB 1; Length 323;
Best Local Similarity 34.3%; Pred. NO. 1.4e-25;
Matches 113; Conservative 61; Mismatches 110; Indels 45; Gaps 14;

QY 36 GDA-HSTIQLCLVSGFSPAKVHVTV- - - - -LVDGQAEALFPVTPRPKEGGQTSLQSE 90
DB 16 GTPSSVTVLGCLVKGILPEPVTVVNSGTLNGVT- - - - -PFSV- - - - -RQSGLYSLSSV 68
QY 91 VNITQGMSSNTYTCHVKH- - - - -NGSIFEDSRKCADSNPR- - - - -GVSAVLRSPSPF 140
DB 69 VSVTS- - - - -SSQVTCNVAHPATNKTVDKTVAPSTCKPTCPPELLGGPSVFIPPKPK 124
QY 141 D-LFIRKSPITICLVVDLAPSKGTNLTW- - - - -SRASGKPVNHSTRKEEKQKQNTLV 193
DB 125 DTLMIKSTPEVTCVVVDVSDQDDEVOFTWYINNEQVTRPPL- - - - -REQQFNSTIRV 178
QY 194 TSLPVGTRDRIEGETYQCRVTHPLFRALMRSTTKLPGRKRLAPEYV-MLPPSPETGT 252
DB 179 VSTLPITHQDLGSKFKCKVHNKALPAPIETISKARGQPLEPKVYTWGPPREELSSRS 238
QY 253 RTVTLIRGYPSEISVQWLFNNEEDHTGHTTTRPKDQDGTDPSEFLYSRLMVKNSIWE 312
DB 239 VSLTCMNGFYPDSIDVWEKNGKAB- - - - -DNYKTPPAVL- - - - -SDGSYFLYNKLSVPTSEWQ 294
QY 313 KGNLVTCTRVVHEALPGSRITLXSLHYSAG 341
DB 295 RGVDFICSVMHEALHNHYT-QKSISSRSPG 322

RESULT 7
GC1_RAT STANDARD; PRT; 326 AA.
AC P20759, 1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0017; PS0017.
DR HSSP; P01842; 7FAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 112 Hinge.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 27 82 Interchain (with a heavy chain).
FT DISULFID 102 102 Interchain (with a heavy chain).
FT DISULFID 106 106 Interchain (with a heavy chain).
FT DISULFID 109 109 Interchain (with a heavy chain).
FT DISULFID 111 111 Interchain (with a heavy chain).
FT DISULFID 140 200
FT DISULFID 246 304


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FT CARBOHYD 176 176 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match      23.5%; Score 436.5; DB 1; Length 326;
Best Local Similarity 32.7%; Pred. No. 1.7e-25;
Matches 105; Conservative 54; Mismatches 131; Indels 31; Gaps 10;

QY 38 AHSTIQLCLVSGFSPAKVHVW----LVDGQEAENLFPYTRPKRGQTFSLQSEVNI 93
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 19 SNSMVLGLCVKGYFPEPTVWNSGALSSG---VHTFPAVLQ-----SGLYTLSSVTV 70

QY 94 TQGNWSSNTYCHVKGNSIFE-----DSSRKCADSNPRGVSAYLSRSPFD- 141
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 71 PSTW-PSQVTCNVAHPASSTKVDKKVPRNCGGDKPCICTGSEVSVFIPPKPKDV 129

QY 142 LFIKSPITICLVLDLAPSKGTVNLTWASRASKPVNHSRKEEKORNGTLTITSLPYGT 201
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 LITLTPKVTVCVVDISQDDPEVHFSWFVDDVEVHTAQTRPEEQFNSTFRSVSELPILH 189

QY 202 RDWIEGTQCRVTHPLPALMRSTTKLPGRKLAPEVMLPSPBEE-TGTRTVTCLIR 260
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 190 QDWLNRTFRCKVTSAAFPSPIEKTIISKDEGRVQPHVVTMGPTTKEENTQNEVSTCMVK 249

QY 261 GFVPSBISVQWLFNNEEDHTGHTTTRPKQDHTGTPSPFLYGRMLVNSIWEKGNLVTCR 320
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 250 GYFPPDIYVQWQNGQPOE--NYKNTPTPTMD--TDCSYFLYKLVNKKKQWQGNFTICS 305

QY 321 VVHEALPGSRTEKSLHYAG 341
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 306 VLHEGLHNHT-EKSLSHSPG 325

RESULT 8
GCC_RAT      STANDARD;      PRT;      329 AA.
AC P20762;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2C chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88166903; PubMed=3127222;
RA Bruggemann M., Delmastro-Galfré P., Waldmann H., Calabi F.;
RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant region
cDNA: extensive homology to mouse gamma 3.";
RL Eur. J. Immunol. 18:317-319(1988).
CC -----
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CC -----
CC EMBL; X07189; CAA30169.1; -.
DR F1R; S00847; S00847.
DR HSP; P01864; IBOG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00407; IGLc1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON TER 1 97
   DOMAIN 1 CH1.

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FT DOMAIN 98 113 Hinge.
FT DOMAIN 114 222 CH2.
FT DOMAIN 223 329 CH3.
FT DISULFID 15 15 Interchain (with a light chain).
FT DISULFID 27 82
FT DISULFID 111 111 Interchain (with a heavy chain).
FT DISULFID 113 113 Interchain (with a heavy chain).
FT DISULFID 143 203
FT DISULFID 249 307
SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;

Query Match      23.1%; Score 428; DB 1; Length 329;
Best Local Similarity 32.4%; Pred. No. 7.8e-25;
Matches 110; Conservative 59; Mismatches 134; Indels 36; Gaps 13;

QY 23 PTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW----LVDGQEAENLFPYTRPK 78
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 PSVYPLVPGCS--GTSGLVTLGLCVKGYFPEPTVWNSGALSSG---VHTFPAVLQ-- 58

QY 79 REGQTFSLQSEVNITOGQMSNTYCHVKH-----NGSIFEDSSRK-----CA-D 124
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 ---SGLYTLSSSVTPSSTW--SSQTVTCSVAHPATKSNLIKRIEPRRPKRPPTDICSD 114

QY 125 SNRPGVSAYLSRSPFD-LFIKSPITICLVLDLAPSKGTVNLTWASRASKPVNHSRKE 183
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 115 DNLGRPSVFIIPKPKDILMITTPKVTVCVVDVSEEDPVQFSWFDVNRVFTAQTPH 174

QY 184 EKQRNGTLTITSLPVGRDMEGTQYQCRVTHPLPALMRSTTKLPGRKLAPEVYMLP 243
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 175 EEQLNGTFRVSTLIHQDWMGSKPEKCKVNNKOLPSPIEKTIKPRGRKARTPQVYTP 234

QY 244 PSPEGTGTR-TVTCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQDHTGTPSPFLYS 302
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 PPREQMSKNKVSUICMTVTSFYPASISVEWERNLEQ--DYKNTLPVLD--SDSEYFLYS 290

QY 303 RMLVNSIWEKGNLVTCRVVHEALPGSRTEKSLHYAG 341
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 291 KLSVDTDSWVRGDIYICSVVHEALHNHT-QKNLSRSPG 328

RESULT 9
GCC2_CAVPO      STANDARD;      PRT;      329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE OF 4-68.
RA MEDLINE=71058471; PubMed=5538606;
RA Birshtein B.K., Husbain Q.Z., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig immunoglobulin-
G(2). 3. Amino acid sequence of the region around the half-cystine
joining heavy and light chains.";
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig immunoglobulin-
G(2). II. Amino acid sequence of the carboxyl-terminal and hinge
region cyanogen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN [4]

```

SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
antibodies.";
RL Biochemistry 13:4796-4803(1974).
RN [5]
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
antibodies.";
RL Biochemistry 13:4804-4811(1974).
RN [6]
DISULFIDE BONDS.
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:28-31(1971).
RN [5]
CC -!- MISCELLANEOUS: This chain was isolated from pooled serum of strain
13 inbred guinea pigs.
CC PIR; A94553; G2GP.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGL1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Direct protein sequencing; Glycoprotein; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON_TER 1 1
FT DISULFID 16 16 Interchain (with a light chain).
FT DISULFID 28 79
FT DISULFID 105 105 Interchain (with a heavy chain).
FT DISULFID 107 107 Interchain (with a heavy chain).
FT DISULFID 110 110 Interchain (with a heavy chain).
FT DISULFID 142 202
FT DISULFID 178 178 N-linked (GlcNAc...).
FT CARBOHYD 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 22.9%; Score 424.5; DB 1; Length 329;
Best Local Similarity 33.2%; Pred. No. 1.4e-24;
Matches 115; Conservative 52; Mismatches 136; Indels 43; Gaps 13;

QY 19- TIPTPVKLFHSCDPRGDAHSTIQLLVSGFSPAKVHTW----LVDGQAEHLPPYT 74
Db 4 TTAPSVFPLAASCVDTSQ---SMWTGLCLVKGYPPEPVTVKNSGALTSQ---VHTFPV 57

QY 75 TRPKRGGTFSIQSVNLTQGMSSNTYTCVHKNGSIFEDSSR----- 120
Db 58 LQ-----SGLYLSTVTVP-----SSQATCNVAHPASSTKVDKTVPIRTPZBPCTC 107

QY 121 -KC-ADSNPRGVSAYLSRSPFD-LPIKSPITICLVLDLAPSKGTVNLTSRSGKPV- 176
Db 108 PKCPPPENLGGPSVFIFPKPKDLMISLTPVTCVVDVSQDEPEVOFTWF-VDNKPVG 166

QY 177 NHSTRKEQRNGTLVTSTLPGVTDTEGTYOCTVTHPLRALMSTTKLPKGLA 236
Db 167 NAETKPRVQYNTFFRVESVLPFHQDMLRGKFKCKVYNKALPAIEKTSKTKGAPRM 226

QY 237 PEVYMLPPPEETGTR-TVTCILIRGFPSEISVQWLFNNEEDHTCHHTTRPOKDHGD 295
Db 227 PDVYTLPPSRDELKSKSVTCLINFFPADIHVEWASNRVPVSEKEYKNTPEID--AD 284

QY 296 PSFFLYSRLMVLNYSIWEKGNLTCTRVVHEALPGSRTLEKSLHYSAG 341
Db 285 GSFLYLSKLTVDKSAWDDQGVVTCVSWHEALNHNVT-QKAISRSPG 329

RESULT 10

GCAB MOUSE STANDARD; PRT; 335 AA.
ID GCAB_MOUSE
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Ig gamma-2A chain C region secreted form (B allele).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Strosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy chain
Fc regions of Ig1a and Ig1b allotypic forms.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- ALTERNATIVE PRODUCTS.
CC -!- Event=Alternative splicing; Named isoforms=2;
CC Names=Secreted;
CC IsoId=P01864-1; Sequence=Displayed;
CC Note=Probably the major isoform;
CC Name=Membrane-bound;
CC IsoId=P01865-1; Sequence=External;
CC -!- MISCELLANEOUS: The sequence differs from that of the a allele,
from BALB/c mice, at 15% of the positions.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.

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entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
or send an email to license@isb-sib.ch).

CC EMBL; J00479; -; NOT ANNOTATED_CDS.
DR PIR; A02153; G2MSAB.
DR PDB; 1BOG; X-ray; B=1-101.
DR PDB; 1HHG; X-ray; B=1-101.
DR PDB; 1HH9; X-ray; B=1-101.
DR PDB; 1HH6; X-ray; B=1-101.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW 3D-structure; Alternative splicing; Direct protein sequencing;
KW Immunoglobulin C region; Immunoglobulin domain; Repeat.

FT NON_TER 1 1
FT DOMAIN 6 98 Ig-like 1.
FT DOMAIN 126 225 Ig-like 2.
FT DOMAIN 234 330 Ig-like 3.
FT STRAND 4 4
FT STRAND 7 11
FT STRAND 22 33
FT STRAND 38 41
FT TURN 42 45
FT TURN 46 46
FT TURN 48 49
FT STRAND 50 52
FT STRAND 56 58
FT TURN 59 60

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FT STRAND 61 71
FT TURN 72 77
FT STRAND 81 86
FT HELIX 87 89
FT TURN 90 90
FT STRAND 91 96
SQ SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;

Query Match 22.7%; Score 421; DB 1; Length 335;
Best Local Similarity 31.7%; Pred. No. 2.7e-24;
Matches 106; Conservative 54; Mismatches 124; Indels 50; Gaps 9;

QY 36 GDAHSTIQLCLVSGSPAKVHVW----LVGQEAENLPYTRPKREGGTFSLQSSV 91
DB 17 GTTGSSTLGLVKGYFPPVTLTWNSGSLSSGVH-----TPALLQSGLYTLSSSV 68
QY 92 NITQGGMSNTVTCVKNGSIFEDSSKCADSNR----- 128
DB 69 TVTSNTW-SQITTCNVHPAS-----STKVDKIEPRVPIQNCPHPORVPPCAAPDL 123
QY 129 -GVSAVLSRFPSPD-LFIRKSPITICLVVDLAPSKGTNLVTSRASGKPVNHSRKEEKQ 186
DB 124 GGSVFIFPKIKDVLMSLSPWTCVVVDSEDDFDVQISFVNNVEVHTAQOTHRD 183
QY 187 RNCGLTVSTLPGTRDWEGETYQCRVTHPLPALMRSTTKLPCKRLAPVYMLPSP 246
DB 184 YNSTLWVSLPIQHODWMSGKEFKCKVNNRALPSPIKTIKPRGPVRAPOVYVLP 243
QY 247 EE-TGTRTVTCILRGFYPSEISVQWLFNNEEDHTGHTTTRPQKHGTDGDFSELYSRML 305
DB 244 EMTKEFSLTCWITGLFAETAVDWTSGRTQYKNTATVLD-----SDGSYFWYSKLR 299
QY 306 VNKSIEKGNLTVCRVHPALPG---SRTLEKSL 336
DB 300 VOKSTWERSLFACVSVHVLNHLTKTISRSL 333

RESULT 11
GC1_MOUSE STANDARD; PRT; 324 AA.
AC P01868;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig gamma-1 chain C region secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX MEDLINE=80202559; PubMed=6769752;
RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
cloned in a bacterial plasmid.";
RL Gene 9:87-97(1980).
RN [3]
RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=80012837; PubMed=113776;
RA Rogers J., Clarke P., Salser W.;
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
heavy chain.";
RL Nucleic Acids Res. 6:3305-3321(1979).
RN [4]

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RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=78242288; PubMed=98524;
RA Adetugbo K.;
RT "Evolution of immunoglobulin subclasses. Primary structure of a murine
myeloma gamma1 chain.";
RL J. Biol. Chem. 253:6068-6075(1978).
RN [5]
RP DISULFIDE BONDS (MOPC 21).
RX MEDLINE=73008889; PubMed=5073237;
RA Svasti J., Milstein C.;
RT "The disulfide bridges of a mouse immunoglobulin G1 protein.";
RL Biochem. J. 126:837-850(1972).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=Secreted;
CC IsoId=P01868-1; Sequence=Displayed;
CC Note=May be the major isoform;
CC Name=Membrane-bound;
CC IsoId=P01869-1; Sequence=External;
CC -----
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or send an email to license@sib-sib.ch).
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EMBL: J00453; AB59656.1; -
EMBL: V00795; CAA24176.1; -
PIR: A02159; GIMS.
GlycoSuiteDB; P01868; -
MGD; MGI:96446; Igh-4.
DR GO: GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO: GO:0003823; P:antigen binding; IDA.
DR GO: GO:0019733; P:antibacterial humoral response (sensu Vertebrata); IDA.
DR GO: GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.
DR GO: GO:0006958; P:complement activation, classical pathway; IDA.
DR GO: GO:0042830; P:defense response to pathogenic bacteria; IDA.
DR GO: GO:0016064; P:humoral defense mechanism (sensu Vertebrata); IDA.
DR GO: GO:0005078; P:negative regulation of inflammatory response; IDA.
DR GO: GO:0006910; P:phagocytosis, binding; IDA.
DR GO: GO:0006911; P:phagocytosis, engulfment; IDA.
DR GO: GO:0005078; P:positive regulation of immune response; IDA.
DR GO: GO:0005079; P:positive regulation of inflammatory response; IDA.
DR GO: GO:0005076; P:positive regulation of phagocytosis; IDA.
DR GO: GO:0016068; P:type I hypersensitivity; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PSS0835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Alternative splicing; Direct protein sequencing; Glycoprotein;
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 110 Hinge.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82 Interchain (with a light chain).
FT DISULFID 102 102 Interchain (with a heavy chain).
FT DISULFID 104 104 Interchain (with a heavy chain).
FT DISULFID 107 107 Interchain (with a heavy chain).
FT DISULFID 109 109 Interchain (with a heavy chain).
FT DISULFID 138 198 N-linked (GLCNAC...).
FT CARBOHYD 174 174 /FTID=CAR_000055.
FT FT 244 302
FT DISULFID 276 276 N -> D (in Ref. 3).
FT CONFLICT 278 278 N -> D (in Ref. 3).
FT CONFLICT 278 278 N -> D (in Ref. 3).
SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;

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Query Match	22.4%	Score 415.5	DB 1	Length 324
Best Local Similarity	31.6%	Pred. No. 7e-24		
Matches	106	Conservative	60	Mismatches 138; Indels 31; Gaps 12
QY	22	PPTVKLPHSSCDPRGDAHSTIQLLCLVSGFSPAKYHVTV	---	LVDGOEAEMLPYITRP 77
DD	5	PPSV--YPLAPGSAQAQNSGWTIGCLVKGYPFEPVTVTWSGSLSG	---	WHTFPAVLQ- 58
QY	78	KREGGQTFSLQSEVNIITQGGWSSNTYTCVHKHGS	-----	IFDSSRK-CADSNPR 128
DD	59	---SDLYTLSSSVTVPSR-RESEVTCNVAHPASSTVKDKI	VPDRCGCKPCICTVPE 113	
QY	129	GVSAYLRSRPFDF-LFTRKSPPTTICLVDLAPSKGTYNLTWSR	AGKPVNHSRKEEKOR 187	
DD	114	VSSVFIIPPFPKQVLITLTLPKTCVVDISKDDPEVQFSWF	VDDVEVHTAQTPRESQF 173	
QY	188	NGTLTVTSTLPVGRDMIEGETVQCRVTHPLPALMRSTTKLP	GGKRLAPEVYMLPPSPE 247	
DD	174	NSTRSVSEIPIHQDWLNKEFKCRVSNAPAPIEKTI	STKGRKPAQVITIPPEKE 233	
QY	248	ETGTTR-TVTCLINGFYPSPISVQWLFNNEEDHTGHTTTR	QKDHGDTPDFFLYSRMLV 306	
DD	234	QMAQKVSILTCMITDFFPDITVEWQNGQP--AENYKNTQPI	MN--TNGSYFYVSKLVN 289	
QY	307	NKSTWEKGNLTVCRVVEHALPGSRTEKSLHVSAG	341	
DD	290	QKSNWEAGNTFTCSVLHEGLNHHT-EKLSHSFG	323	

RESULT 12

ID	GC3_HUMAN	STANDARD	PRT	230 AA.
AC	P01860;			
DD	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	IG gamma-3 chain C region (Heavy chain disease protein) (HDC).			
DE	Name=IGHG3;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RN	SEQUENCE (DISEASE PROTEIN WIS).			
RX	MEDLINE=81021548; PubMed=6774747;			
RA	Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;			
RT	"Primary structure of human gamma 3 immunoglobulin deletion mutant:			
RT	gamma 3 heavy-chain disease protein Wis.;"			
RRL	Biochemistry 19:4304-4308(1980).			
RN	[2]			
RN	REVIEWS TO 12-97 (PROTEIN WIS).			
RX	MEDLINE=77118561; PubMed=402363;			
RX	Michaelson T.E., Frangione B., Franklin E.C.;			
RA	"Primary structure of the 'hinge' region of human IgG3. Probable			
RT	quadruplication of a 15-amino acid residue basic unit.;"			
RL	J. Biol. Chem. 252:883-889(1977).			
RN	[3]			
RN	REVIEWS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC).			
RX	MEDLINE=77021516; PubMed=823945;			
RX	Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;			
RA	"The amino acid sequence of 'heavy chain disease' protein ZUC.			
RT	Structure of the FC fragment of immunoglobulin G3.;"			
RT	Biochem. Biophys. Res. Commun. 71:907-914(1976).			
RL	[4]			
RN	SEQUENCE FROM N.A. (DISEASE PROTEIN OWM).			
RX	MEDLINE=82247635; PubMed=6608505;			
RX	Alexander A., Steinmetz M., Barrिताult D., Frangione B.,			
RA	Franklin E.C., Hood L., Buxbaum J.N.;"			
RT	"Gamma Heavy chain disease in man: cDNA sequence supports partial gene			
RT	deletion model.;"			
RL	Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).			
CC	!- SUBUNIT: Dimer linked by 12 disulfide bonds; it has an extra			
CC	interchain disulfide bond at position 7 in addition to the 11			

SQ SEQUENCE 290 AA; 32331 MW; E69CBC95705B2F46 CRC64;
 Query Match 21.6%; Score 401.5; DB 1; Length 290;
 Best Local Similarity 39.5%; Pred. No. 7.3e-23;
 Matches 85; Conservative 49; Mismatches 74; Indels 7; Gaps 5;
 QY 129 GVSAYLSRSPED-LFIRKSPITCLVPLAPSKGVNLTWSRSGKPVNHSRKEKOR 187
 DB 80 GPSVFLFPKPKDTLMISFEVTCVVDVSHEDDEVQFKYVDGVQVNAKTPREQOF 139
 QY 188 NGTLVTSTLPVGTWISGEYQCRVTHPHLPRALMRSTTKLPGRKLAPEVYMLPPSPPE 247
 DB 140 NSTFRVSVLTQLHQLWDLGKEYCKVSNKALPAPIEKTIISKQPREPQVYTLPPSRE 199
 QY 248 E-TGTRTCTCLIRGYPSEISVQWLFNNEEDHTGHHTTRPKQDHGTDPSFELYSRLV 306
 DB 200 EMTKNOVSTCLVKGYPSDIAVEMSSQPN--NYNTTPMLD--SDGSFFLYSKLTV 255
 QY 307 NKSIWEKGNLTCRVVHEALPGSRITLEKSLHSYASG 341
 DB 256 DKSRWQGNIFSCVMHEAL-HNRFTQKSLSLSPG 289
 RESULT 13
 GCB MOUSE STANDARD; PRT; 336 AA.
 ID GCB_MOUSE AC P01866;
 DT 21-JUL-1986 (Rel. 01.' Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE 19 gamma-2B chain C region secreted form.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ALLELE A).
 RX MEDLINE=801207116; PubMed=6766534;
 RA Yamawaki-Kataoka Y., Kataoka T., Takahashi N., Obata M., Honjo T.;
 RT "Complete nucleotide sequence of immunoglobulin gamma2b chain gene
 RT cloned from newborn mouse DNA.";
 RL Nature 283:786-789(1980).
 RN [2]
 RP SEQUENCE FROM N.A. (MPC 11).
 RX MEDLINE=80081501; PubMed=117548;
 RA Tucker P.W., Marcu K.B., Slighcom J.L., Blattner F.R.;
 RT "Structure of the constant and 3' untranslated regions of the murine
 RT gamma 2b heavy chain messenger RNA.";
 RL Science 206:1299-1303(1979).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80081502; PubMed=117549;
 RA Tucker P.W., Marcu K.B., Newell N., Richards J., Blattner F.R.;
 RT "Sequence of the cloned gene for the constant region of murine gamma
 RT 2b immunoglobulin heavy chain.";
 RL Science 206:1303-1306(1979).
 RN [4]
 RP SEQUENCE FROM N.A. (ALLELE B).
 RX MEDLINE=82173203; PubMed=6803173;
 RA Ollo R., Rougeon F.;
 RT "Mouse immunoglobulin allotypes: post-duplication divergence of gamma
 RT 2a and gamma 2b chain genes.";
 RL Nature 296:761-763(1982).
 RN [5]
 RP CARBOHYDRATE-LINKAGE SITE THR-105.
 RX MEDLINE=94216359; PubMed=7512967;
 RA Kim H., Yamaguchi Y., Masuda K., Matsunaga C., Yamamoto K.,
 RA Irimura T., Takahashi N., Kato K., Arata Y.;
 RT "O-Glycosylation in hinge region of mouse immunoglobulin G2b.";
 RL J. Biol. Chem. 269:12345-12350(1994).
 CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;

CC Name=Secreted;
 CC IsoId=P01866-1; Sequence=Displayed;
 CC Note=May be the major isoform;
 CC Name=Membrane-bound;
 CC IsoId=P01867-1; Sequence=External;
 CC PTM: O-linked glycan consists of Gal-GalNAc disaccharide which is
 CC modified with 2 sialic acid residues.
 CC -!- MISCELLANEOUS: The a allele sequence is shown.
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
 DR PIR: S25057; G2MS11.
 DR HSSP: P01867; 1CIC.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; ig; 3.
 DR PROSITE: PS00835; IG-LIKE; 3.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR Alternative splicing; Glycoprotein; Immunoglobulin C region;
 KW Immunoglobulin domain; Repeat.
 FT NON_TER 1 1
 FT DOMAIN 6 98 Ig-like 1.
 FT DOMAIN 127 226 Ig-like 2.
 FT DOMAIN 235 331 Ig-like 3.
 FT DISULFID 15 15 Interchain (with a light chain) (By
 FT similarity).
 FT DISULFID 27 82 By similarity.
 FT DISULFID 109 109 Interchain (with a heavy chain) (By
 FT similarity).
 FT DISULFID 112 112 Interchain (with a heavy chain) (By
 FT similarity).
 FT DISULFID 115 115 Interchain (with a heavy chain) (By
 FT similarity).
 FT DISULFID 118 118 Interchain (with a heavy chain) (By
 FT similarity).
 FT DISULFID 150 210 By similarity.
 FT DISULFID 256 314 By similarity.
 FT CARBOHYD 105 105 O-linked (GalNAc...).
 FT VARIANT 163 163 Q -> R (in allele B).
 FT VARIANT 194 194 T -> A (in allele B).
 FT VARIANT 300 300 M -> D (in allele B).
 FT VARIANT 301 301 N -> I (in allele B).
 FT CONFLICT 25 25 L -> S (in Ref. 2 and 3).
 FT CONFLICT 36 36 S -> P (in Ref. 2 and 3).
 FT CONFLICT 239 239 I -> T (in Ref. 2 and 3).
 SQ SEQUENCE 336 AA; 7D879662607C356E CRC64;
 Query Match 21.5%; Score 399.5; DB 1; Length 336;
 Best Local Similarity 31.1%; Pred. No. 1.3e-22;
 Matches 107; Conservative 61; Mismatches 139; Indels 37; Gaps 13;
 QY 22 PPTVKLFHSSCDPRGD-AHSTIQLCLVSGFSAKVHVTVLWDGQAEALFPYTTTPKRE 80
 DB 5 PPSVYPLAPGC--GDTTSSVTGLCLVKGYPFESVTVTW-NSGSLSSSVH---TPFALL 57
 QY 81 GGQTFSLQSEVNITQGGOMSSNTVTHVKINGSI-----FEDSS-----R 120
 DB 58 QSGLYTMSSSVTPSSTW-PSQIVTCSVAHPASTIVDKLEPSGPISTINPCFPCKECH 116
 QY 121 KCADSN-PRGVAYLSRSPFD-LFTRKSPITCLVVDLAPSKGTNLTWSRSGKPVNH 178
 DB 117 KCPAPNLEGGPSVFIFPPNIKVDLMISLTPKTVCVVDVSEDDPDVQISFVANNVEVHTA 176
 QY 179 STRKEEKQRNGTLVTSTLPVGTWISGEYQCRVTHPHLPRALMRSTTKLPGRKLAPE 238
 DB 177 QTQTHREDYNSTRVSTLFIHQDWNWSEKFKCKVNNKDLPSPIERTISKIQLVRAPQ 236
 QY 239 VYMLPPSPFEETGTR-TVTCLIRGYPSEISVQWLFNNEEDHTGHHTTRPKQDHGTDPS 297
 DB 237 VYILPPPAEQLSRKDVSLTCLVGVNPGDISVWTSNGHTEE--NYKDTAPVLD--SDGS 292
 QY 298 FFYYSRMLVNSKWEKGNLTCRVVHEALPGSRITLEKSLHSYASG 341
 DB 293 YFYISKLNMTSKWEKTDSPSCNVRHEGLK-NYYLKRKTSRSPG 335


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DR SMART; SMO0407; IGc1; 2.
DR PROSITE; PS50835; IG LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW 3D-structure; Immunoglobulin C region; Immunoglobulin domain; Repeat.
FT NON_TER 1
FT DOMAIN 6 98 Ig-like 1.
FT DOMAIN 121 220 Ig-like 2.
FT DOMAIN 229 325 Ig-like 3.
FT DISULFID 15 15 Interchain (with a light chain).
FT DISULFID 27 82
FT DISULFID 107 107 Interchain (with a heavy chain).
FT DISULFID 110 110 Interchain (with a heavy chain).
FT DISULFID 112 112 Interchain (with a heavy chain).
FT DISULFID 144 204
FT DISULFID 250 308
FT STRAND 4 4
FT STRAND 7 11
FT STRAND 22 33
FT STRAND 38 41
FT HELIX 42 44
FT TURN 45 45
FT STRAND 46 46
FT STRAND 50 52
FT STRAND 56 56
FT TURN 59 60
FT STRAND 62 71
FT TURN 72 77
FT STRAND 81 86
FT HELIX 87 89
FT TURN 90 90
FT STRAND 91 96
SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match 21.3%; Score 395.5; DB 1; Length 330;
Best Local Similarity 31.7%; Pred. No. 2.5e-22;
Matches 104; Conservative 55; Mismatches 124; Indels 45; Gaps 12;

QY 40 STIQLLCLVSGSPAKVHTW---LVDGQEAENLPYTPRKREGGQTFSLQSEVNTIQ 95
Db 21 SSVTLGLVKGYPPEPVTLTWNGSLSSG---VHTPPAVLQ-----SDYTLSSSVTVTS 72

QY 96 GQMSNTYTCYKHNGSIFEDSSRXCADSNPRGSA-----YLSRPSPF--- 140
Db 73 STW-PSQITCNVHPAS---STKVDKKIEPRGPTIKPCPKCPAPNLLGGPSVFIPP 127

QY 141 -----DLPIRKSPTITCLVVDLAPSKGTYNLTWSRAGKPVNHSRKEKQKNGILTITS 195
Db 128 PKIKOVLMSLSPIVTCVVVDVSEDDPDVQISGFVNNVEVHTAQIQTHREDYNSTLRVYS 187

QY 196 TLPVGRDRIEGTYOCRTHPHLPALMRSTTKLPGRKLAPVYMLPPSPPEETGTTR-- 253
Db 188 ALPIQHODMWSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLP-PEENTKKQV 246

QY 254 TVTCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQDHGTDPSFPLYSRMLVNKSIWEK 313
Db 247 TLTGMVTDMPEDIYVEWTNNGKTEL--NYKNTPEVLD--SDGSYFMYSKLAVEKKNWVE 302

QY 314 GNLVTCRVVHEALPGSRITLKSILHYSAG 341
Db 303 RNSYSCSVVHGLNHHHT-TKSFSPITP 329
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Search completed: November 14, 2004, 15:05:26
Job time : 98 secs

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Db 162 TREKNTV-STHSELNITQGEWSQKTYTCQVYQGTFTKDEARKCSSESDPRGVTSYLSPP 220
QY 138 SPFDLFIKSPITICLVVDLAKSGTGNLTWSRAGSKPVNHSTRKEEQRKQRTLTVTSTL 197
Db 221 SPDLVYHAKPKITICLVWDLATMEG-MNLTWYRESKEPVNPGPLNKKDHFNGTITVTSTL 279
QY 198 PVGTRDWIEGETYQCRVTHPHLPALMRSTTKLPKRLAPEVYMLPPSPPEETGTR--TV 255
Db 280 PVNTNDWIEGETYQCRVTHPHLPKDIVRSIAKAPGRAPPDVYLFLLPPEEGQTKDRVTL 339
QY 256 TCLIRGFYPSSEISVQWLFNNEEDHTGHTTTTPQKDHGTDPSFFLYSRMLVNKSIWEKGN 315
Db 340 TCLIQNFFPADISVQWLRNDSPIQDQYTTTGHKVGSRPAFFIFSRLEVSRLVDMQKN 399
QY 316 LVTCRVVHEALPGSRITLKSLSHVSAG 341
Db 400 KFTCQVVEALSGSRILQKWVSKTPG 425

RESULT 2

PCT-US95-13795-2
; Sequence 2, Application PC/TUS9513795
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE, P.O. BOX 2000
; CITY: RARITON
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13795
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-13795-2

Query Match 53.3%; Score 989; DB 5; Length 426;
Best Local Similarity 56.7%; Pred. No. 1.3e-87;
Matches 185; Conservative 53; Mismatches 84; Indels 4; Gaps 3;

QY 18 VTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTLWVDGQAEALPFTYTRP 77
Db 102 LNFIPPTVKLFHSSCNFVGTHTTITQLCLISGVYVPGDMEVTLWVDGQKATNIFPYTAPG 161
QY 78 KREGGOTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSRKCADSNPRGVSAYLSRP 137
Db 162 TREKNTV-STHSELNITQGEWSQKTYTCQVYQGTFTKDEARKCSSESDPRGVTSYLSPP 220
QY 138 SPFDLFIKSPITICLVVDLAKSGTGNLTWSRAGSKPVNHSTRKEEQRKQRTLTVTSTL 197

Db 221 SPDLVYHAKPKITICLVWDLATMEG-MNLTWYRESKEPVNPGPLNKKDHFNGTITVTSTL 279
QY 198 PVGTRDWIEGETYQCRVTHPHLPALMRSTTKLPKRLAPEVYMLPPSPPEETGTR--TV 255
Db 280 PVNTNDWIEGETYQCRVTHPHLPKDIVRSIAKAPGRAPPDVYLFLLPPEEGQTKDRVTL 339
QY 256 TCLIRGFYPSSEISVQWLFNNEEDHTGHTTTTPQKDHGTDPSFFLYSRMLVNKSIWEKGN 315
Db 340 TCLIQNFFPADISVQWLRNDSPIQDQYTTTGHKVGSRPAFFIFSRLEVSRLVDMQKN 399
QY 316 LVTCRVVHEALPGSRITLKSLSHVSAG 341
Db 400 KFTCQVVEALSGSRILQKWVSKTPG 425

RESULT 3

US-09-479-614-14
; Sequence 14, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-14

Query Match 52.4%; Score 972; DB 4; Length 431;
Best Local Similarity 56.7%; Pred. No. 5.9e-86;
Matches 185; Conservative 52; Mismatches 85; Indels 4; Gaps 4;

QY 18 VTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTLWVDGQAEALPFTYTRP 77
Db 107 LNFIPPTVKLFHSSCNFVGTHTTITQLCLISGVYVPGDMEVTLWVDGQKATNIFPYTAPG 166
QY 78 KREGGOTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSRKCADSNPRGVSAYLSRP 137
Db 167 KQEGKVT-STHSELNITQGEWSQKTYTCQVYQGTFTEDHARKCTESDPRGVSAYLSPP 225
QY 138 SPFDLFIKSPITICLVVDLAKSGTGNLTWSRAGSKPVNHSTRKEEQRKQRTLTVTSTL 197
Db 226 SPDLVYHAKPKITICLVWDLATMEG-LTWSRENGESVHPDPMVKKTQYNGTITVTSTL 284
QY 198 PVGTRDWIEGETYQCRVTHPHLPALMRSTTKLPKRLAPEVYMLPPSPPEETGTR--TV 255
Db 285 PVDATDWEGETYQCRVTHPHLPKDIVRSIAKAPGRAPPDVYLFLLPPEEGQTKDRVTL 344
QY 256 TCLIRGFYPSSEISVQWLFNNEEDHTGHTTTTPQKDHGTDPSFFLYSRMLVNKSIWEKGN 315
Db 345 TCLIQNFFPADISVQWLRNDSPIQDQYTTTGHKVGSRPAFFIFSRLEVSRLVDMQKN 404
QY 316 LVTCRVVHEALPGSRITLKSLSHVSAG 341
Db 405 VFTCQVVEALPGSRITLKSLSHVSAG 430

RESULT 4

US-09-479-614-2
; Sequence 2, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric

```

; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
; US-09-479-614-2

Query Match 52.4%; Score 972; DB 4; Length 496;
Best Local Similarity 56.7%; Pred. No. 7.3e-86;
Matches 185; Conservative 52; Mismatches 85; Indels 4; Gaps 4

QY 18 VTIIPTVKLPHSSCDPRGDAHSIIQLCLVSGSPAKVHVTLVVGQBAENLFPYTRP 77
DB 172 MNFIPTVKLPHSSCNPLGDTGSIQLCLISGVPGDMEVTLVVGQKATNIFPYTAP 231
QY 78 KREGGQTSLOSEVNITOGWMSNTYTCHVKNGSTFEDSSRKCADSNPRGVSAYLGRP 137
DB 232 KEGKVT-STHSELNITOGWMSVSKTYTCVYQGTTFEDHAKCTESDPRGVSYILSP 290
QY 138 SPFDLPIRKSPITICLVVDLAPSKGTVNLTWMSRAGKPVNHSRKEEKORNGTLVTSTL 197
DB 291 SPLDLVYVHKSPKITCLVVDLANTDGM-TLWSRENGESVHPDPMWKTQYNGTITVTSTL 349
QY 198 PVGTEDWVEGETYQCRVTHPLPRALMRSTIKLPGKRLABEVTM-LPPSP-ETGTTTV 255
DB 350 PVDATDWVEGETYQCKVTHPLDKDIVRSIAKAPGRFPPEVYVFLPPEGEPTKDKVIL 409
QY 256 TCLIRGFPSSETSVOWLFNNEEDTGHHTTTRPOKDHGTDPSFFLYSRMLVNKSIWEKGN 315
DB 410 TCLIQNFPPDISVOWLHNDSPVTEQQATTWPHKATGSPFAFVFSRLEVSADWEQD 469
QY 316 LVTCRVVHEALPGSRTLEKSLHYSAG 341
DB 470 VFTCOVVHEALPGFRTLAKKYSKKNPG 495

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RESULT 5
US-09-479-614-29
; Sequence 29, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-29

Query Match 52.4%; Score 972; DB 4; Length 496;
Best Local Similarity 56.7%; Pred. No. 7,3e-86;
Matches 185; Conservative 52; Mismatches 85; Indels 4; Gaps 4

Qy 18 VIIIIPTVKLFHSSCDPRGDAHSITQLCLVSGFSPAKVHTVLVDGQAEHLFPYTTTP 77
Db 172 MNFIPTVKLFHSSCNPLGDTGTSTQLLCLISGVPGDMETVLVDGQKATNIFPYTAP 231
Qy 78 KREGGOTFSLQSEVNITQOMSSNTYTCHVKHNGSIFEDSSRRKCADSNPRGVSAVLSRP 137

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Db      232 KQSGKV-TSHSEINITQGEVWQKTYTCQVTQGTFEDHARKCTESDPRGVSTYLSPP 290
Qy      138 SPFDLFIRKSPTTICLVVDIAPSKGTVNLTWSRASGPKPVNHSTRKEEKQRNGTLTVTSTL 197
Db      291 SPLDYVHKSPKITCLVVDIANTDGM-I-LTWSRENGESVHPDPMPVKTKQYNGTIIVTSTL 349
Qy      198 PVGTWDIEGETQCRRVTHPHLPALMRSTTKPLGKRLAPEVYM-LPSPB-ETGTTRTV 255
Db      350 PVDATDWVEGETQCKVTHFDLPKDIVRSIAKAPGRFPFVEVVFLPPEGEPTKDKVIL 409
Qy      256 TCIIRGYPSSEISVOMLFNNEEDHTGHHTTRPOKHGTDPSFFLYSRMLVNKSIWEKN 315
Db      410 TCIIONFPFPDISVOMLNHNSPVRTQQOATTPHEKATGPSAFPVFVRLEVSRADEQRD 469
Qy      316 LVTCRVVHEALPGSRTLEKSLHSYAG 341
Db      470 VFCQVVEHALPGFRLLKXSVKNKP 495

RESULT 6
US-09-192-545-2
; Sequence 2, Application US/09192545
; Patent No. 6118044
; GENERAL INFORMATION:
; APPLICANT: Katasuyama, Hajime
; APPLICANT: Yonekawa, Hiromichi
; APPLICANT: Taya, Choji
; APPLICANT: Matsuoaka, Kunie
; TITLE OF INVENTION: Transgenic Animal Allergy Models and Methods for Their Use
; FILE REFERENCE: 799P79570
; CURRENT APPLICATION NUMBER: US/09/192,545
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: JP HEI 9-313989
; EARLIER FILING DATE: 1997-11-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 561
; TYPE: PRM
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: Designed heavy
US-09-192-545-2

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Query Match	36.3%	Score	673;	DB	3;	Length	561;
Best Local Similarity	41.6%	Pred. No.	1e-56;				
Matches	147;	Conservative	53;	Mismatches	133;	Indels	20;
Gaps	7;						

Qy	2	FHHHHHTLSLPSGPGVTIIPPTVKLPHS-----SCDPGRDAHSTIQLLCLVSGF	51
Db	211	FTCHVTHPPGPNESRTHLVRPVT---HSUSPPWSYSIHRCDPNA-FHSTIQLCYFVGH	265
Qy	52	SPAKVHVTVLWDGQEAENLPYTRPRREGQTFSLQSEVNITOGQWSSNTYTCVHKHN	111
Db	266	ILNDVSYSWMLDREIIDTLAQTVLKEE-GKLASTCKLNIITQQWSESTFFICRVTSQ	324
Qy	112	GSIFEDSSRKCAQSNPRGVSAYLSRSPGFDLFRKSPITICLVVDLAPSKGTVNLWTRA	171
Db	325	GVDYLAHTRRCPOHPEPRGAIYTIPLPSPLDLYQNGAPKLTCLVVDLESEK-NVNVNTNQE	383
Qy	172	SGRPVNHSTRKEEQKNGTLTVTSTLVGTRDTEGETYQCRVTHPLPALMRSTTKLP	231
Db	384	KKTSVSASQWYTKHHNNWATTSITSLPVAKWDLEGYQCVVDROPFPKPIVRSIT-LP	442
Qy	232	--GKRLAPEVVMPLPPSPPEETGTTVTVCLIRGFPYPSISQWLFPNNBEDHTGHHTTRPQ	289
Db	443	QVSQSAPEVYVFPPEESSEDKRTLCLCNFPEDISVQWLGDGKLINSQHSITITPL	502
Qy	290	KDHGTDPSTFLYSRLMKNYSIWEGKNILVTRVHEALPGSRTLSEKSLHYSAGN	342
Db	503	KSGNSGOGFTIFSLEVAKTLWTKORKOFTCOVIEHALQPKRKLEKTTSTSLGN	555

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RESULT 7
US-08-232-539D-56
; Sequence 56, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Ige Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,539D
; FILING DATE: 21-Apr-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-232-539D-56
Query Match 31.2%; Score 579; DB 2; Length 113;
Best Local Similarity 98.2%; Pred. No. 1.3e-48;
Matches 109; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 122 CADSPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSTR 181
Db 1 CADSPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSTR 60

Qy 182 KEKORNGTLTVTSTLPVGTTRDWIEGETYQCRVTHPHLPRALMRSTTKLPG 232
Db 61 KEKORNGTLTVTSTLPVGTTRDWIEGETYQCRVTHPHLPRALMRSTTKTSG 111

RESULT 8
US-08-466-163B-1
; Sequence 1, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26

Query Match 29.6%; Score 548.5; DB 3; Length 109;
Best Local Similarity 97.2%; Pred. No. 1.1e-45;
Matches 106; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 124 DSNPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSTR 183
Db 1 DSNPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSTR 60

Qy 184 EKORNGTLTVTSTLPVGTTRDWIEGETYQCRVTHPHLPRALMRSTTKLPG 232
Db 61 EKORNGTLTVTSTLPVGTTRDWIEGETYQCRVTHPHLPRALMRSTTKTSG 108

RESULT 9
US-09-802-096-1
; Sequence 1, Application US/09802096
; Patent No. 6685939
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 1
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-096-1
Query Match 29.6%; Score 548.5; DB 4; Length 109;
Best Local Similarity 97.2%; Pred. No. 1.1e-45;
Matches 106; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 124 DSNPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSTR 183
Db 1 DSNPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSTR 60

Qy 184 EKORNGTLTVTSTLPVGTTRDWIEGETYQCRVTHPHLPRALMRSTTKLPG 232
Db 61 EKORNGTLTVTSTLPVGTTRDWIEGETYQCRVTHPHLPRALMRSTTKTSG 108

RESULT 10
US-09-802-077-1
; Sequence 1, Application US/09802077
; Patent No. 669472
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
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/ FILE REFERENCE: P0718P2C2US
/ CURRENT APPLICATION NUMBER: US/09/802,077
/ CURRENT FILING DATE: 2001-03-08
/ PRIOR APPLICATION NUMBER: US 08/405,617
/ PRIOR FILING DATE: 1995-03-15
/ PRIOR APPLICATION NUMBER: US 08/185,899
/ PRIOR FILING DATE: 1994-01-26
/ PRIOR APPLICATION NUMBER: PCT/US92/06860
/ PRIOR FILING DATE: 1992-08-14
/ PRIOR APPLICATION NUMBER: US 07/879,495
/ PRIOR FILING DATE: 1992-05-07
/ PRIOR APPLICATION NUMBER: US 07/744,768
/ PRIOR FILING DATE: 1991-08-14
/ NUMBER OF SEQ ID NOS: 64
/ SEQ ID NO 1
/ LENGTH: 109
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-802-077-1

Query Match      29.6%; Score 548.5; DB 4; Length 109;
Best Local Similarity 97.2%; Pred. No. 1.1e-45;
Matches 106; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 124 DSNPRGVSAYLSRPSFDFIRKSPITICLVVDLAPSKGTNLTWSRAGKPVNHSRKE 183
Db 1 DSNPRGVSAYLSRPSFDFIRKSPITICLVVDLAPSKGTNLTWSRAGKPVNHSRKE 60

QY 184 EKORNGTLAVTSTLPVGTDRDIEGETYQCRVTHPHLPALMESTTKLPG 232
Db 61 EKORNGTLAVTSTLPVGTDRDIEGET-QCRVTHPHLPALMESTTKTSG 108

RESULT 11
US-08-232-539D-54
/ Sequence 54, Application US/08232539D
/ Patent No. 5965709
/ GENERAL INFORMATION:
/ APPLICANT: Presta, Leonard G.
/ APPLICANT: Jardieu, Paula M.
/ TITLE OF INVENTION: Ige Antagonists
/ NUMBER OF SEQUENCES: 60
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WinPatIn (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/232,539D
/ FILING DATE: 21-Apr-1994
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/178583
/ FILING DATE: 07-JAN-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/744768
/ FILING DATE: 14-AUG-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Svoboda, Craig G.
/ REGISTRATION NUMBER: 39,044
/ REFERENCE/DOCKET NUMBER: P0718P3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-1489
/ TELEFAX: 650/952-9881
/ INFORMATION FOR SEQ ID NO: 54:
/ SEQUENCE CHARACTERISTICS:
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/ LENGTH: 106 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
US-08-232-539D-54

Query Match      29.0%; Score 538; DB 2; Length 106;
Best Local Similarity 98.1%; Pred. No. 1.1e-44;
Matches 102; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 129 GVSAYLSRPSFDFIRKSPITICLVVDLAPSKGTNLTWSRAGKPVNHSRKEKQRN 188
Db 1 GVSAYLSRPSFDFIRKSPITICLVVDLAPSKGTNLTWSRAGKPVNHSRKEKQRN 60

QY 189 GTLTVTSTLPVGTDRDIEGETYQCRVTHPHLPALMESTTKLPG 232
Db 61 GTLTVTSTLPVGTDRDIEGETYQCRVTHPHLPALMESTTKTSG 104

RESULT 12
US-09-828-995B-38
/ Sequence 38, Application US/09828995B
/ Patent No. 6703360
/ GENERAL INFORMATION:
/ APPLICANT: Heska Corporation
/ APPLICANT: McCall, Catherine A.
/ APPLICANT: Tang, Liang A.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE Igg AND CANINE IL-13
/ FILE REFERENCE: AL-7
/ CURRENT APPLICATION NUMBER: US/09/828,995B
/ CURRENT FILING DATE: 2001-04-09
/ PRIOR APPLICATION NUMBER: 60/195,874
/ PRIOR FILING DATE: 2000-04-07
/ PRIOR APPLICATION NUMBER: 60/195,859
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 104
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 38
/ LENGTH: 352
/ TYPE: PRT
/ ORGANISM: Canis familiaris
US-09-828-995B-38

Query Match      28.0%; Score 520.5; DB 4; Length 352;
Best Local Similarity 36.4%; Pred. No. 3.4e-42;
Matches 129; Conservative 58; Mismatches 138; Indels 29; Gaps 12;

QY 5 HHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTWLVDG 64
Db 10 HWNGTSLFVSSASTTAPSVFPLAPSCGSTG---STVALACLVSgyfppfvtswnsds 66

QY 65 -QEAEENLFPYTRPKREGGQTFSLQSEVNITQGWMSNTYTCHVKHNGS-----IFE 116
Db 67 LTSGVHTFPVSVL-----QSSGLYLSLSSTVTPSSRW-PSEFTCNVHPASNTKVDKEVPK 121

QY 117 DSSRKCADSNP-----RGVSAYLSRPSFDFIRKSPITICLVVDLAPSKGTNLTWSR 170
Db 122 ESTCKCISPCVPVPSLGGPSVFIPPPKDKILRTRTPEITCVVLDLGDREDPEVQISWF- 180

QY 171 ASGRPVNHS-TRKEEKQRNGTLVTSTLPVGTDRDIEGETYQCRVTHPHLPALMESTTK 229
Db 181 VDGKEVHTAKTPREQQFNSTYRVSVLPIEHQDWLTGKFKCRKRNHIGLPSFIERTISK 240

QY 230 LPGRKLAPEVYMLPPSPPEE--TGTRTAVTCLIRGFYPSSEISVQWLFNNEEDHTGHTTTR 287
Db 241 ARGQAQPSVYVLPFPPSPKELSSSDTVTLTCLDKDFPPEIDVEWQNSGQPEPEKHYHTA 300

QY 288 PQKDHTGTDPSFFLYSRMLVNSIWEKGNLVTCTRVVHEALPGSRITLESLSLHYSAG 341
Db 301 PQLDE--DGSYFLYSKLSVDKSRWQQDPFTCAVMEALQNHYT-DLSLSHSPG 351

RESULT 13
US-09-828-995B-11
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Sequence 11, Application US/09828995B
Patent No. 6703360
GENERAL INFORMATION:
APPLICANT: Heskia Corporation
APPLICANT: McCall, Catherine A.
APPLICANT: Tang, Liang A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13 R
FILE REFERENCE: AL-7
CURRENT APPLICATION NUMBER: US/09/828,995B
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 60/195,874
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/195,659
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patent in version 3.1
SEQ ID NO 11
LENGTH: 470
TYPE: PRT
ORGANISM: Canis familiaris
US-09-828-995B-11

Query Match 28.0%; Score 519.5; DB 4; Length 470;
Best Local Similarity 36.4%; Pred. No. 6.5e-42;
Matches 130; Conservative 58; Mismatches 134; Indels 35; Gaps 13;

QY 5 HHHHTLSLPSGPTVITPTVKLFHSSCDPRGDHSTIQLLCLVSGFSPAKVHTW---- 60
DB 128 HWNGTSLFVSSASTAPVFLAPSCGSTG---STVALACLVSGYFPEPTVSVNWSGS 184
QY 61 LVDGQAEALFPYTRPKEGGTSLSQEVNITQCOMSSNTYCHVKHGS----- 113
DB 185 LTSG---VHTFPSVL-----QSSGLXLSSTVVPSSRW-PSETFTCNVHPASNTKVKDP 236
QY 114 IFEDSRKCADSNP-----RGVSAYLSRSPDLP-IRKSPITCLVDLAPSKGTNLT 167
DB 237 VPKESTCKISPCVPESLGFSVFIFPPPKDILIRITPTVTCVLDLGRDEPEVQIS 296
QY 168 WSRASGKPVNHS--TRKEKORNGTLVTSTLPVGTDRDTEGETYOCRTVHPHLPALMRS 226
DB 297 WF-VDSKEVHTAKTQPREQFNSYRVVSVLPIEHQDMLTGKFKCRVNHICLPSPERT 355
QY 227 TTKLPGRKLAPVYMLPPSPER--TGTTTTCVLRGYPSPISVQWLFNNEEDHTGHT 284
DB 356 ISKARGQAHQPSVYVLPSPKELSSSDTITLCLIKDFYPPDIDVEWQSQGQPEPESKYH 415
QY 285 TTRPOKHGTDPSFFLYSRMLYNKSTWEGNLVTCRVVHEALPGSRTLEKSLHYSAG 341
DB 416 TTAPOQDE--DGSYFLYSLVDSKRWQGGDTFTCAVMHETLQNHYT-DLSLSHSPG 469

RESULT 14
US-09-828-995B-5
Sequence 5, Application US/09828995B
Patent No. 6703360
GENERAL INFORMATION:
APPLICANT: Heskia Corporation
APPLICANT: McCall, Catherine A.
APPLICANT: Tang, Liang A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13 R
FILE REFERENCE: AL-7
CURRENT APPLICATION NUMBER: US/09/828,995B
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 60/195,874
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/195,659
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patent in version 3.1
SEQ ID NO 5
LENGTH: 468
TYPE: PRT
ORGANISM: Canis familiaris

US-09-828-995B-5
Query Match 27.6%; Score 513; DB 4; Length 468;
Best Local Similarity 36.4%; Pred. No. 2.8e-41;
Matches 124; Conservative 58; Mismatches 121; Indels 38; Gaps 14;

QY 23 PTVKLFHSSCDPRGDHSTIQLLCLVSGFSPAKVHTW----LVDGQAEALFPYTRPK 78
DB 143 PSVFPLAPSCG--STGSLVALACLVSGYFPEPTVSVNWSGSLSG---VHTFPSVL--- 194
QY 79 REGQTFPSLQSEVNITQCOMSSNTYCHVKHGS-----IFEDSRKCADSNP----- 127
DB 195 -QSSGLXLSSTVVPSSRW-PSETFTCNVHPASNTKVKDPVFNEC--RCITDTPCPVP 250
QY 128 ---RGVSAYLSRSPDLP-IRKSPITCLVDLAPSKGTNLTWGRASGKPVNHS--TRK 182
DB 251 EPLGGPSVLIFPPPKDILIRITPTVTCVLDLGRDEPEVQISWF-VDSKEVHTAKTOS 309
QY 183 BEKORNGTLVTSTLPVGTDRDTEGETYOCRTVHPHLPALMRS--TKLPGRKLAPVYML 242
DB 310 REQFNGTYRVVSVLPIEHQDMLTGKFKCRVNHICLPSPERTISKARGRAHKPSVYVL 369
QY 243 PPSEETGTTTIV--TCLIRGYPSPISVQWLFNNEEDHTGHTTTRPOKHGTDPSFPL 300
DB 370 PPSPKELSSSDTITLCLIKDFYPPDIDVEWQSQGQPEPEKHMTPPQOLDE--DGSYFL 427
QY 301 YSRMLYNKSTWEGNLVTCRVVHEALPGSRTLEKSLHYSAG 341
DB 428 YKSLVDSKRWQGGDTFTCAVMHETLQNHYT-DLSLSHSPG 467

RESULT 15
US-08-646-981-16
Sequence 16, Application US/08646981
Patent No. 5852183
GENERAL INFORMATION:
APPLICANT: MAEDA, HIROAKI
APPLICANT: EDA, YASUYUKI
APPLICANT: KINACHI, KAZUHIKO
APPLICANT: ONO, YOICHI
APPLICANT: TOKIYOSHI, SACHIO
TITLE OF INVENTION: DOG-MOUSE HETEROHYBRIDOMA AND GENE
TITLE OF INVENTION: FRAGMENT CODING FOR CONSTANT REGION OF CANINE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,981
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1488-106
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 334 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-646-981-16

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Query Match      27.6%; Score 512; DB 2; Length 334;
Best Local Similarity 35.9%; Pred. No. 2.1e-41;
Matches 123; Conservative 60; Mismatches 122; Indels 38; Gaps 12;

QY 23 PTVKLPSSCDPRGDAHSIIQLLLCLVSGFSPAKVHVW----LVDQGEAENLFPVYTRPK 78
Db 5 PSVFPLDPSCG--STSGSIVALACLVSgyfpepVIVSWNSGSLTSG-----VHTFPSD 55

QY 79 REGGQTFSLQSEVNITQGGWMSNTYTCHVKH-----NGSIFE--DSSRK 121
Db 56 LQSSGLYSLSSMVTVPSSRW--SSEFTCNVAHPASKTKVDKVPKRENGRVRPRPDCPKC 114

QY 122 CADSNPRGVSAYLSRSPFD-LPIKSPITICLVVDLAPSKGTVNLTWASRSGKPVNHS- 179
Db 115 PAPMLGGPSVFIFPKPKDTHLIARTPEVTCVVVDLGPEDPEVQISWF-VDGKQNTAK 173

QY 180 TRKEEQRTGLTVITLPGVTRDMIEGETYQCRVTHPLPRALMRSTTKLFGKELAPEV 239
Db 174 TQPREQFNGTVRVSVLPIGHQDMLKGKQFTCKVNNKALPSPIERTISKARGQAHPQSV 233

QY 240 YMLPPSPER-TGTRTVTCLIRGFYFSEISVONLFNNEEDHTGHTTTPQKHGTDPSF 298
Db 234 YVLPSPRELSKNTVSLTCLIKDFPDDIDVWQSNQOQEPESKYRTTTPPQLDE--DGSY 291

QY 299 FLYSRMLVNKSIWEKGNLVTCRVVHEALPGSRTEKSLHYSAG 341
Db 292 FLYSKLSVDKSRWQRGDTFICAWHEALHNHYT-QKSLSHSPG 333
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Search completed: November 14, 2004, 15:03:00
Job time : 40 secs

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OM protein - protein search, using sw model
Run on: November 14, 2004, 15:01:45 ; Search time 144 Seconds
(without alignments)
840.320 Million cell updates/sec

Title: US-09-401-636-8
Perfect score: 1856
Sequence: 1 EFHHHHHTLSLPESGVTI.....HEALPGRSTLEKSLHYSAGN 342
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1568699 seqs, 353819137 residues
Total number of hits satisfying chosen parameters: 1568699
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pdb:
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pdb:
3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pdb:
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pdb:
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pdb:
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pdb:
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pdb:
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pdb:
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pdb:
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pdb:
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pdb:
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pdb:
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pdb:
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pdb:
15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pdb:
16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pdb:
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pdb:
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pdb:
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pdb:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
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1	1856	100.0	342 9 US-09-401-636-8
2	1856	100.0	342 14 US-10-176-664-8
3	1856	100.0	342 15 US-10-673-594-8
4	1786	96.2	338 15 US-10-438-794-6
5	1786	96.2	338 15 US-10-453-915-6
6	1786	96.2	337 15 US-10-438-794-14
7	1786	96.2	347 15 US-10-453-915-14
8	1772	95.5	557 15 US-10-438-794-12
9	1772	95.5	557 15 US-10-438-794-16
10	1772	95.5	557 15 US-10-453-915-12
11	1772	95.5	557 15 US-10-453-915-16
12	1772	95.5	556 15 US-10-438-794-10
13	1772	95.5	556 15 US-10-438-794-18

14	1772	95.5	566	15	US-10-453-915-10	Sequence 10, Appl
15	1772	95.5	566	15	US-10-453-915-18	Sequence 18, Appl
16	1759	94.8	353	15	US-10-453-915-21	Sequence 21, Appl
17	1644.5	88.6	341	9	US-09-401-636-11	Sequence 11, Appl
18	1644.5	88.6	341	14	US-10-176-664-11	Sequence 3, Appl
19	1644.5	88.6	341	15	US-10-673-594-11	Sequence 11, Appl
20	1587.5	85.5	341	9	US-09-401-636-3	Sequence 3, Appl
21	1587.5	85.5	341	14	US-10-176-664-3	Sequence 3, Appl
22	1587.5	85.5	341	15	US-10-673-594-3	Sequence 3, Appl
23	1587.5	85.5	345	9	US-09-401-636-10	Sequence 10, Appl
24	1587.5	85.5	345	14	US-10-176-664-10	Sequence 10, Appl
25	1587.5	85.5	345	15	US-10-673-594-10	Sequence 10, Appl
26	1568.5	84.5	341	9	US-09-401-636-9	Sequence 9, Appl
27	1568.5	84.5	341	14	US-10-176-664-9	Sequence 9, Appl
28	1568.5	84.5	341	15	US-10-673-594-9	Sequence 9, Appl
29	1553.5	83.7	341	9	US-09-401-636-4	Sequence 4, Appl
30	1553.5	83.7	341	14	US-10-176-664-4	Sequence 4, Appl
31	1553.5	83.7	341	15	US-10-673-594-4	Sequence 4, Appl
32	1528.5	82.4	341	9	US-09-401-636-6	Sequence 6, Appl
33	1528.5	82.4	341	14	US-10-176-664-6	Sequence 6, Appl
34	1528.5	82.4	341	15	US-10-673-594-6	Sequence 6, Appl
35	1523.5	82.1	446	14	US-10-214-524-32	Sequence 32, Appl
36	1519	81.8	342	9	US-09-401-636-5	Sequence 5, Appl
37	1519	81.8	342	14	US-10-176-664-5	Sequence 5, Appl
38	1519	81.8	342	15	US-10-673-594-5	Sequence 5, Appl
39	1498.5	80.7	337	15	US-10-438-794-3	Sequence 3, Appl
40	1498.5	80.7	337	15	US-10-453-915-3	Sequence 3, Appl
41	1486.5	80.1	555	15	US-10-438-794-8	Sequence 8, Appl
42	1486.5	80.1	555	15	US-10-453-915-8	Sequence 8, Appl
43	1285.5	69.3	427	14	US-10-214-524-36	Sequence 36, Appl
44	1050.5	56.6	343	9	US-09-401-636-7	Sequence 7, Appl
45	1050.5	56.6	343	14	US-10-176-664-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-401-636-8
; Sequence 8, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401.636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-8

Query Match	100.0%	Score 1856;	DB 9;	Length 342;
Best Local Similarity	100.0%	Pred. No. 1.5e-139;		
Matches 342;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	EFHHHHHTLSLPESGVTIIPPTVKLFHSCDPRGDAHSTIQLLCLVSGFSPAKVHTW	60	
DB	1	EFHHHHHTLSLPESGVTIIPPTVKLFHSCDPRGDAHSTIQLLCLVSGFSPAKVHTW	60	
QY	61	LVDQEAENFPYTRPKREGGQTFSLQSEVNTQGMSSNTYCHVKNGSIFEDSSR	120	
DB	61	LVDQEAENFPYTRPKREGGQTFSLQSEVNTQGMSSNTYCHVKNGSIFEDSSR	120	
QY	121	KCADSNRGYSAYLSRSPDLFTRKSPITCLVVDLAPSKGTNLTWSRSGKPVNHS	180	

Db 121 KCADSNPRGVSAYLSRPSDFLFIKSPITITCLVLDLAPSKGTVNLVTSRASGKPVNHST 180
 QY 181 RKEEKQRNGTLTVSTLPVGTDRWIEGETYQCRVTHPHLPALMRSTTKLPGRKLAPEVY 240
 Db 181 RKEEKQRNGTLTVSTLPVGTDRWIEGETYQCRVTHPHLPALMRSTTKLPGRKLAPEVY 240
 QY 241 MLPSPPEETGTTTRVTCCLIRGFYPSISVQWLFNNEEDHTGHTTTRPKQKHGTDPSPFL 300
 Db 241 MLPSPPEETGTTTRVTCCLIRGFYPSISVQWLFNNEEDHTGHTTTRPKQKHGTDPSPFL 300
 QY 301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
 Db 301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342

RESULT 2

US-10-176-664-8
 ; Sequence 8, Application US/10176664
 ; Publication No. US20030031663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hellman, Lars T.
 ; TITLE OF INVENTION: ENHANCED VACCINES
 ; FILE REFERENCE: 10223/006001
 ; CURRENT APPLICATION NUMBER: US/10/176,664
 ; CURRENT FILING DATE: 2002-06-19
 ; PRIOR APPLICATION NUMBER: US/09/401,636
 ; PRIOR FILING DATE: 1999-09-22
 ; PRIOR APPLICATION NUMBER: US 60/106,652
 ; PRIOR FILING DATE: 1998-11-02
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Fast-Seq for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 342
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetically generated proteins
 US-10-176-664-8

Query Match 100.0%; Score 1856; DB 14; Length 342;
 Best Local Similarity 100.0%; Pred. No. 1.5e-139;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60
 Db 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60
 QY 61 LVDGQAEANLFPYTTTRPKREGGOTFSQSEVNIQGWSSNTYTCVHKHNGSIFEDSSR 120
 Db 61 LVDGQAEANLFPYTTTRPKREGGOTFSQSEVNIQGWSSNTYTCVHKHNGSIFEDSSR 120
 QY 121 KCADSNPRGVSAYLSRPSDFLFIKSPITITCLVLDLAPSKGTVNLVTSRASGKPVNHST 180
 Db 121 KCADSNPRGVSAYLSRPSDFLFIKSPITITCLVLDLAPSKGTVNLVTSRASGKPVNHST 180
 QY 181 RKEEKQRNGTLTVSTLPVGTDRWIEGETYQCRVTHPHLPALMRSTTKLPGRKLAPEVY 240
 Db 181 RKEEKQRNGTLTVSTLPVGTDRWIEGETYQCRVTHPHLPALMRSTTKLPGRKLAPEVY 240
 QY 241 MLPSPPEETGTTTRVTCCLIRGFYPSISVQWLFNNEEDHTGHTTTRPKQKHGTDPSPFL 300
 Db 241 MLPSPPEETGTTTRVTCCLIRGFYPSISVQWLFNNEEDHTGHTTTRPKQKHGTDPSPFL 300
 QY 301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
 Db 301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342

RESULT 3

US-10-673-594-8
 ; Sequence 8, Application US/10673594
 ; Publication No. US20040076625A1
 ; GENERAL INFORMATION:

; APPLICANT: Hellman, Lars T.
 ; TITLE OF INVENTION: ENHANCED VACCINES
 ; FILE REFERENCE: 10223/006001
 ; CURRENT APPLICATION NUMBER: US/10/673,594
 ; CURRENT FILING DATE: 2003-09-29
 ; PRIOR APPLICATION NUMBER: US/09/401,636
 ; PRIOR FILING DATE: 1999-09-22
 ; PRIOR APPLICATION NUMBER: US 60/106,652
 ; PRIOR FILING DATE: 1998-11-02
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Fast-Seq for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 342
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetically generated proteins
 US-10-673-594-8

Query Match 100.0%; Score 1856; DB 15; Length 342;
 Best Local Similarity 100.0%; Pred. No. 1.5e-139;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60
 Db 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60
 QY 61 LVDGQAEANLFPYTTTRPKREGGOTFSQSEVNIQGWSSNTYTCVHKHNGSIFEDSSR 120
 Db 61 LVDGQAEANLFPYTTTRPKREGGOTFSQSEVNIQGWSSNTYTCVHKHNGSIFEDSSR 120
 QY 121 KCADSNPRGVSAYLSRPSDFLFIKSPITITCLVLDLAPSKGTVNLVTSRASGKPVNHST 180
 Db 121 KCADSNPRGVSAYLSRPSDFLFIKSPITITCLVLDLAPSKGTVNLVTSRASGKPVNHST 180
 QY 181 RKEEKQRNGTLTVSTLPVGTDRWIEGETYQCRVTHPHLPALMRSTTKLPGRKLAPEVY 240
 Db 181 RKEEKQRNGTLTVSTLPVGTDRWIEGETYQCRVTHPHLPALMRSTTKLPGRKLAPEVY 240
 QY 241 MLPSPPEETGTTTRVTCCLIRGFYPSISVQWLFNNEEDHTGHTTTRPKQKHGTDPSPFL 300
 Db 241 MLPSPPEETGTTTRVTCCLIRGFYPSISVQWLFNNEEDHTGHTTTRPKQKHGTDPSPFL 300
 QY 301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
 Db 301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342

RESULT 4

US-10-438-794-6
 ; Sequence 6, Application US/10438794
 ; Publication No. US20040038395A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LUNDGREN, Mats
 ; APPLICANT: FUENTES, Alexis
 ; APPLICANT: MAGNUSON, Ann-Christin
 ; TITLE OF INVENTION: Chimeric ige Polypeptides and Host Cells
 ; FILE REFERENCE: 10223-017001
 ; CURRENT APPLICATION NUMBER: US/10/438,794
 ; CURRENT FILING DATE: 2003-05-15
 ; PRIOR APPLICATION NUMBER: US 60/382,552
 ; PRIOR FILING DATE: 2002-05-21
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: Fast-Seq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 338
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic polypeptide designated OSO
 US-10-438-794-6

Query Match

96.2%; Score 1786; DB 15; Length 338;

```
Best Local Similarity 99.4%; Pred. No. 5.7e-134;
Matches 334; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 9 TSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTLVLDGQAE 68
DB 3 TSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTLVLDGQAE 62
QY 69 NLPFYTRPKREGGQTFSLQSEVNITQGWMSNTYTCHVKNGSIFEDSSRKCADSNPR 128
DB 63 NLPFYTRPKREGGQTFSLQSEVNITQGWMSNTYTCHVKNGSIFEDSSRKCADSNPR 122
QY 129 GVSAYLSRSPDFLIRKSPITICLVVDLAPSGVTNLVWSRSGKPVNHSRKEEKORN 188
DB 123 GVSAYLSRSPDFLIRKSPITICLVVDLAPSGVTNLVWSRSGKPVNHSRKEEKORN 182
QY 189 GTLVTSTLPVGRDWEIETGYQCRVTHPLPALMRSTTKL--PGKRLAPEVYMLPPSP 246
DB 183 GTLVTSTLPVGRDWEIETGYQCRVTHPLPALMRSTTKLASPGKRLAPEVYMLPPSP 242
QY 247 EETGTRTIVTCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQDGTDPSPFLYSRLV 306
DB 243 EETGTRTIVTCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQDGTDPSPFLYSRLV 302
QY 307 NKSIWEKGNLVTGCRVHEALPGSRTLEKSLHYSAGN 342
DB 303 NKSIWEKGNLVTGCRVHEALPGSRTLEKSLHYSAGN 338

RESULT 5
US-10-453-915-6
; Sequence 6, Application US/10453915
; Publication No. US20040054146A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; APPLICANT: Persson, Stefan
; APPLICANT: Jansson, Asa
; TITLE OF INVENTION: Allergy Vaccines
; FILE REFERENCE: 10223-008001
; CURRENT APPLICATION NUMBER: US/10/453,915
; PRIOR FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: 60/408,648
; PRIOR FILING DATE: 2002-09-05
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric polypeptide
US-10-453-915-6

Query Match 96.2%; Score 1786; DB 15; Length 338;
Best Local Similarity 99.4%; Pred. No. 5.7e-134;
Matches 334; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 9 TSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTLVLDGQAE 68
DB 3 TSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTLVLDGQAE 62
QY 69 NLPFYTRPKREGGQTFSLQSEVNITQGWMSNTYTCHVKNGSIFEDSSRKCADSNPR 128
DB 63 NLPFYTRPKREGGQTFSLQSEVNITQGWMSNTYTCHVKNGSIFEDSSRKCADSNPR 122
QY 129 GVSAYLSRSPDFLIRKSPITICLVVDLAPSGVTNLVWSRSGKPVNHSRKEEKORN 188
DB 123 GVSAYLSRSPDFLIRKSPITICLVVDLAPSGVTNLVWSRSGKPVNHSRKEEKORN 182
QY 189 GTLVTSTLPVGRDWEIETGYQCRVTHPLPALMRSTTKL--PGKRLAPEVYMLPPSP 246
DB 183 GTLVTSTLPVGRDWEIETGYQCRVTHPLPALMRSTTKLASPGKRLAPEVYMLPPSP 242
QY 247 EETGTRTIVTCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQDGTDPSPFLYSRLV 306
DB 243 EETGTRTIVTCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQDGTDPSPFLYSRLV 302
QY 307 NKSIWEKGNLVTGCRVHEALPGSRTLEKSLHYSAGN 342
DB 303 NKSIWEKGNLVTGCRVHEALPGSRTLEKSLHYSAGN 338

RESULT 6
US-10-438-794-14
; Sequence 14, Application US/10438794
; Publication No. US20040038395A1
; GENERAL INFORMATION:
; APPLICANT: LUNDGREN, Mats
; APPLICANT: FUENTES, Alexis
; APPLICANT: MAGNUSON, Ann-Christin
; TITLE OF INVENTION: Chimeric IGE Polypeptides and Host Cells
; FILE REFERENCE: 10223-017001
; CURRENT APPLICATION NUMBER: US/10/438,794
; CURRENT FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/382,552
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide designated OSO-H
US-10-438-794-14

Query Match 96.2%; Score 1786; DB 15; Length 347;
Best Local Similarity 99.4%; Pred. No. 5.9e-134;
Matches 334; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 9 TSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTLVLDGQAE 68
DB 3 TSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTLVLDGQAE 62
QY 69 NLPFYTRPKREGGQTFSLQSEVNITQGWMSNTYTCHVKNGSIFEDSSRKCADSNPR 128
DB 63 NLPFYTRPKREGGQTFSLQSEVNITQGWMSNTYTCHVKNGSIFEDSSRKCADSNPR 122
QY 129 GVSAYLSRSPDFLIRKSPITICLVVDLAPSGVTNLVWSRSGKPVNHSRKEEKORN 188
DB 123 GVSAYLSRSPDFLIRKSPITICLVVDLAPSGVTNLVWSRSGKPVNHSRKEEKORN 182
QY 189 GTLVTSTLPVGRDWEIETGYQCRVTHPLPALMRSTTKL--PGKRLAPEVYMLPPSP 246
DB 183 GTLVTSTLPVGRDWEIETGYQCRVTHPLPALMRSTTKLASPGKRLAPEVYMLPPSP 242
QY 247 EETGTRTIVTCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQDGTDPSPFLYSRLV 306
DB 243 EETGTRTIVTCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQDGTDPSPFLYSRLV 302
QY 307 NKSIWEKGNLVTGCRVHEALPGSRTLEKSLHYSAGN 342
DB 303 NKSIWEKGNLVTGCRVHEALPGSRTLEKSLHYSAGN 338

RESULT 7
US-10-453-915-14
; Sequence 14, Application US/10453915
; Publication No. US20040054146A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; APPLICANT: Persson, Stefan
; APPLICANT: Jansson, Asa
; TITLE OF INVENTION: Allergy Vaccines
; FILE REFERENCE: 10223-008001
; CURRENT APPLICATION NUMBER: US/10/453,915
; CURRENT FILING DATE: 2003-06-02
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; PRIOR APPLICATION NUMBER: 60/408,648
; PRIOR FILING DATE: 2002-09-05
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric polypeptide
US-10-453-915-14

Query Match          96.2%; Score 1786; DB 15; Length 347;
Best Local Similarity 99.4%; Pred. No. 5.9e-134;
Matches 334; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 9 TSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTLVLDGQAE 68
DB 3 TSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTLVLDGQAE 62

QY 69 NLPFYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSRKCADSNPR 128
DB 63 NLPFYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSRKCADSNPR 122

QY 129 GVSAYLSRSPFDLFRKSPITICLVVDLAPSKGTVNLTWASGKPVNHSTRKEEKQRN 188
DB 123 GVSAYLSRSPFDLFRKSPITICLVVDLAPSKGTVNLTWASGKPVNHSTRKEEKQRN 182

QY 189 GTLVSTLPGVTRDIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSP 246
DB 183 GTLVSTLPGVTRDIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSP 242

QY 247 EETGTRTVCILRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFLYSRLMV 306
DB 243 EETGTRTVCILRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFLYSRLMV 302

QY 307 NKSIWEGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
DB 303 NKSIWEGNLVTCRVVHEALPGSRTLEKSLHYSAGN 338

RESULT 8
US-10-438-794-12
; Sequence 12, Application US/10438794
; Publication No. US20040038395A1
; GENERAL INFORMATION:
; APPLICANT: LUNDGREN, Mats
; APPLICANT: FUENTES, Alexis
; APPLICANT: MAGNUSSON, Ann-Christin
; TITLE OF INVENTION: Chimeric Ige Polypeptides and Host Cells
; FILE REFERENCE: 10223-017001
; CURRENT APPLICATION NUMBER: US/10/438,794
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/382,552
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide designated modOSO
US-10-438-794-12

Query Match          95.5%; Score 1772; DB 15; Length 557;
Best Local Similarity 98.5%; Pred. No. 1.4e-132;
Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 LSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTLVLDGQAE 69
DB 225 IDIPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTLVLDGQAE 284

QY 70 LFPYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSRKCADSNPR 129
DB 285 LFPYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSRKCADSNPR 344

QY 130 VSAYLSRSPFDLFRKSPITICLVVDLAPSKGTVNLTWASGKPVNHSTRKEEKQRN 189
DB 345 VSAYLSRSPFDLFRKSPITICLVVDLAPSKGTVNLTWASGKPVNHSTRKEEKQRN 404

QY 190 TLTVTSTLPGVTRDIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSP 249
DB 405 TLTVTSTLPGVTRDIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSP 464

QY 250 GTTTRTVCILRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFLYSRLMV 309
DB 465 GTTTRTVCILRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFLYSRLMV 524

QY 310 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342
DB 525 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 557

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QY 70 LFPYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSRKCADSNPR 129
DB 285 LFPYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSRKCADSNPR 344

QY 130 VSAYLSRSPFDLFRKSPITICLVVDLAPSKGTVNLTWASGKPVNHSTRKEEKQRN 189
DB 345 VSAYLSRSPFDLFRKSPITICLVVDLAPSKGTVNLTWASGKPVNHSTRKEEKQRN 404

QY 190 TLTVTSTLPGVTRDIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSP 249
DB 405 TLTVTSTLPGVTRDIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSP 464

QY 250 GTTTRTVCILRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFLYSRLMV 309
DB 465 GTTTRTVCILRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFLYSRLMV 524

QY 310 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342
DB 525 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 557

RESULT 9
US-10-438-794-16
; Sequence 16, Application US/10438794
; Publication No. US20040038395A1
; GENERAL INFORMATION:
; APPLICANT: LUNDGREN, Mats
; APPLICANT: FUENTES, Alexis
; APPLICANT: MAGNUSSON, Ann-Christin
; TITLE OF INVENTION: Chimeric Ige Polypeptides and Host Cells
; FILE REFERENCE: 10223-017001
; CURRENT APPLICATION NUMBER: US/10/438,794
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/382,552
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide designated OSO
US-10-438-794-16

Query Match          95.5%; Score 1772; DB 15; Length 557;
Best Local Similarity 98.5%; Pred. No. 1.4e-132;
Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 LSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTLVLDGQAE 69
DB 225 IDIPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTLVLDGQAE 284

QY 70 LFPYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSRKCADSNPR 129
DB 285 LFPYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSRKCADSNPR 344

QY 130 VSAYLSRSPFDLFRKSPITICLVVDLAPSKGTVNLTWASGKPVNHSTRKEEKQRN 189
DB 345 VSAYLSRSPFDLFRKSPITICLVVDLAPSKGTVNLTWASGKPVNHSTRKEEKQRN 404

QY 190 TLTVTSTLPGVTRDIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSP 249
DB 405 TLTVTSTLPGVTRDIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSP 464

QY 250 GTTTRTVCILRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFLYSRLMV 309
DB 465 GTTTRTVCILRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFFLYSRLMV 524

QY 310 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342
DB 525 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 557

```

```
RESULT 10
US-10-453-915-12
; Sequence 12, Application US/10453915
; Publication No. US20040054146A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; APPLICANT: Persson, Stefan
; APPLICANT: Jansson, Aea
; TITLE OF INVENTION: Allergy Vaccines
; FILE REFERENCE: 10223-008001
; CURRENT APPLICATION NUMBER: US/10/453,915
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: 60/408,648
; PRIOR FILING DATE: 2002-09-05
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimexic polypeptide
US-10-453-915-12

Query Match      95.5%; Score 1772; DB 15; Length 557;
Best Local Similarity 98.5%; Pred. No. 1.4e-132;
Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 LSLPESGPVTIIPTVKLFHSSCDPRGDAHSITQLLCLVSGFSPAKVHVTVLVDGQEAEN 69
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 225 IDIPESGPVTIIPTVKLFHSSCDPRGDAHSITQLLCLVSGFSPAKVHVTVLVDGQEAEN 284

QY 70 LPYITRPKREGGQTFSLQSEVNITQGMSSNTYTCVHKHNGSIFEDSSRKCADSNPRG 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 285 LPYITRPKREGGQTFSLQSEVNITQGMSSNTYTCVHKHNGSIFEDSSRKCADSNPRG 344

QY 130 VSAVLSRSPFDLFIKSPITITCLVVDLAPSKGTNLTWSRASKGKPVNHSRKEEKQKNG 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 345 VSAVLSRSPFDLFIKSPITITCLVVDLAPSKGTNLTWSRASKGKPVNHSRKEEKQKNG 404

QY 190 TLTVTSTLPVGRDMEGETYQCRVTHPLPALMRSTTKLPKRLAPEVYMLPPSPPEET 249
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 405 TLTVTSTLPVGRDMEGETYQCRVTHPLPALMRSTTKLPKRLAPEVYMLPPSPPEET 464

QY 250 GTTRVTCLIRGYPBSISVQWLFNNEEDHTGHTTTRPOKDHGTDPSFFLYSRMLVNKS 309
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 465 GTTRVTCLIRGYPBSISVQWLFNNEEDHTGHTTTRPOKDHGTDPSFFLYSRMLVNKS 524

QY 310 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 525 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 557

RESULT 11
US-10-453-915-16
; Sequence 16, Application US/10453915
; Publication No. US20040054146A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; APPLICANT: Persson, Stefan
; APPLICANT: Jansson, Aea
; TITLE OF INVENTION: Allergy Vaccines
; FILE REFERENCE: 10223-008001
; CURRENT APPLICATION NUMBER: US/10/453,915
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: 60/408,648
; PRIOR FILING DATE: 2002-09-05
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide designated mcdososo-H
US-10-438-794-10

Query Match      95.5%; Score 1772; DB 15; Length 566;
Best Local Similarity 98.5%; Pred. No. 1.4e-132;
Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 LSLPESGPVTIIPTVKLFHSSCDPRGDAHSITQLLCLVSGFSPAKVHVTVLVDGQEAEN 69
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 225 IDIPESGPVTIIPTVKLFHSSCDPRGDAHSITQLLCLVSGFSPAKVHVTVLVDGQEAEN 284

QY 70 LPYITRPKREGGQTFSLQSEVNITQGMSSNTYTCVHKHNGSIFEDSSRKCADSNPRG 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 285 LPYITRPKREGGQTFSLQSEVNITQGMSSNTYTCVHKHNGSIFEDSSRKCADSNPRG 344

QY 130 VSAVLSRSPFDLFIKSPITITCLVVDLAPSKGTNLTWSRASKGKPVNHSRKEEKQKNG 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 345 VSAVLSRSPFDLFIKSPITITCLVVDLAPSKGTNLTWSRASKGKPVNHSRKEEKQKNG 404

QY 190 TLTVTSTLPVGRDMEGETYQCRVTHPLPALMRSTTKLPKRLAPEVYMLPPSPPEET 249
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 405 TLTVTSTLPVGRDMEGETYQCRVTHPLPALMRSTTKLPKRLAPEVYMLPPSPPEET 464

QY 250 GTTRVTCLIRGYPBSISVQWLFNNEEDHTGHTTTRPOKDHGTDPSFFLYSRMLVNKS 309
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 465 GTTRVTCLIRGYPBSISVQWLFNNEEDHTGHTTTRPOKDHGTDPSFFLYSRMLVNKS 524

QY 310 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 525 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 557
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimexic polypeptide
US-10-453-915-16

Query Match      95.5%; Score 1772; DB 15; Length 557;
Best Local Similarity 98.5%; Pred. No. 1.4e-132;
Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 LSLPESGPVTIIPTVKLFHSSCDPRGDAHSITQLLCLVSGFSPAKVHVTVLVDGQEAEN 69
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 225 IDIPESGPVTIIPTVKLFHSSCDPRGDAHSITQLLCLVSGFSPAKVHVTVLVDGQEAEN 284

QY 70 LPYITRPKREGGQTFSLQSEVNITQGMSSNTYTCVHKHNGSIFEDSSRKCADSNPRG 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 285 LPYITRPKREGGQTFSLQSEVNITQGMSSNTYTCVHKHNGSIFEDSSRKCADSNPRG 344

QY 130 VSAVLSRSPFDLFIKSPITITCLVVDLAPSKGTNLTWSRASKGKPVNHSRKEEKQKNG 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 345 VSAVLSRSPFDLFIKSPITITCLVVDLAPSKGTNLTWSRASKGKPVNHSRKEEKQKNG 404

QY 190 TLTVTSTLPVGRDMEGETYQCRVTHPLPALMRSTTKLPKRLAPEVYMLPPSPPEET 249
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 405 TLTVTSTLPVGRDMEGETYQCRVTHPLPALMRSTTKLPKRLAPEVYMLPPSPPEET 464

QY 250 GTTRVTCLIRGYPBSISVQWLFNNEEDHTGHTTTRPOKDHGTDPSFFLYSRMLVNKS 309
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 465 GTTRVTCLIRGYPBSISVQWLFNNEEDHTGHTTTRPOKDHGTDPSFFLYSRMLVNKS 524

QY 310 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 525 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 557

RESULT 12
US-10-438-794-10
; Sequence 10, Application US/10438794
; Publication No. US20040038395A1
; GENERAL INFORMATION:
; APPLICANT: LUNDGREN, Mats
; APPLICANT: FUENTES, Alexis
; APPLICANT: MAGNUSSON, Ann-Christin
; TITLE OF INVENTION: Chimeric Ige Polypeptides and Host Cells
; FILE REFERENCE: 10223-017001
; CURRENT APPLICATION NUMBER: US/10/438,794
; CURRENT FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/382,552
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 566
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide designated mcdososo-H
US-10-438-794-10

Query Match      95.5%; Score 1772; DB 15; Length 566;
Best Local Similarity 98.5%; Pred. No. 1.4e-132;
Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 LSLPESGPVTIIPTVKLFHSSCDPRGDAHSITQLLCLVSGFSPAKVHVTVLVDGQEAEN 69
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 225 IDIPESGPVTIIPTVKLFHSSCDPRGDAHSITQLLCLVSGFSPAKVHVTVLVDGQEAEN 284

QY 70 LPYITRPKREGGQTFSLQSEVNITQGMSSNTYTCVHKHNGSIFEDSSRKCADSNPRG 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 285 LPYITRPKREGGQTFSLQSEVNITQGMSSNTYTCVHKHNGSIFEDSSRKCADSNPRG 344

QY 130 VSAVLSRSPFDLFIKSPITITCLVVDLAPSKGTNLTWSRASKGKPVNHSRKEEKQKNG 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 345 VSAVLSRSPFDLFIKSPITITCLVVDLAPSKGTNLTWSRASKGKPVNHSRKEEKQKNG 404
```

QY 190 TLTVSTLPGTRDWEGETYQCRVTHPHLPALMRSTTKLPKRLAPEVYMLPPSPPEET 249
Db 405 TLTVSTLPGTRDWEGETYQCRVTHPHLPALMRSTTKLPKRLAPEVYMLPPSPPEET 464
QY 250 GTTRVTCLIRGFYSEISVQWLFNNEEDHTGHTTTTRPKDGHGTDPSFFLYSRMLVNKS 309
Db 465 GTTRVTCLIRGFYSEISVQWLFNNEEDHTGHTTTTRPKDGHGTDPSFFLYSRMLVNKS 524
QY 310 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342
Db 525 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 557

RESULT 13

US-10-438-794-18
; Sequence 18, Application US/10438794
; Publication No. US20040038395A1
; GENERAL INFORMATION:
; APPLICANT: LUNDGREN, Mats
; APPLICANT: FUENTES, Alexis
; APPLICANT: MAGNUSSON, Ann-Christin
; TITLE OF INVENTION: Chimeric Ige Polypeptides and Host Cells
; FILE REFERENCE: 10223-017001
; CURRENT APPLICATION NUMBER: US/10/438,794
; CURRENT FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/382,552
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 566
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide designated OSO50-H
US-10-438-794-18

Query Match 95.5%; Score 1772; DB 15; Length 566;
Best Local Similarity 98.5%; Pred. No. 1.4e-132;
Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 10 LSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTVLVDQAEAN 69
Db 225 IDIPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTVLVDQAEAN 284
QY 70 LPYTRPRKREGGQTFSLQSEVNIITOGQWSSNTVTCVHKHNGSIFEDSSRKCADSNPRG 129
Db 285 LPYTRPRKREGGQTFSLQSEVNIITOGQWSSNTVTCVHKHNGSIFEDSSRKCADSNPRG 344
QY 130 VSAYLSRSPFPDLFIKSPFTIICLVVDLAPSKGTVNLWTSRAGSKPVNHSRKEEKQKNG 189
Db 345 VSAYLSRSPFPDLFIKSPFTIICLVVDLAPSKGTVNLWTSRAGSKPVNHSRKEEKQKNG 404
QY 190 TLTVSTLPGTRDWEGETYQCRVTHPHLPALMRSTTKLPKRLAPEVYMLPPSPPEET 249
Db 405 TLTVSTLPGTRDWEGETYQCRVTHPHLPALMRSTTKLPKRLAPEVYMLPPSPPEET 464
QY 250 GTTRVTCLIRGFYSEISVQWLFNNEEDHTGHTTTTRPKDGHGTDPSFFLYSRMLVNKS 309
Db 465 GTTRVTCLIRGFYSEISVQWLFNNEEDHTGHTTTTRPKDGHGTDPSFFLYSRMLVNKS 524
QY 310 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342
Db 525 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 557

RESULT 14

US-10-453-915-10
; Sequence 10, Application US/10453915
; Publication No. US20040054146A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.

; APPLICANT: Persson, Stefan
; APPLICANT: Jansson, Asa
; TITLE OF INVENTION: Allergy Vaccines
; FILE REFERENCE: 10223-008001
; CURRENT APPLICATION NUMBER: US/10/453,915
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: 60/408,648
; PRIOR FILING DATE: 2002-09-05
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 566
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric polypeptide
US-10-453-915-10

Query Match 95.5%; Score 1772; DB 15; Length 566;
Best Local Similarity 98.5%; Pred. No. 1.4e-132;
Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 10 LSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTVLVDQAEAN 69
Db 225 IDIPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTVLVDQAEAN 284
QY 70 LPYTRPRKREGGQTFSLQSEVNIITOGQWSSNTVTCVHKHNGSIFEDSSRKCADSNPRG 129
Db 285 LPYTRPRKREGGQTFSLQSEVNIITOGQWSSNTVTCVHKHNGSIFEDSSRKCADSNPRG 344
QY 130 VSAYLSRSPFPDLFIKSPFTIICLVVDLAPSKGTVNLWTSRAGSKPVNHSRKEEKQKNG 189
Db 345 VSAYLSRSPFPDLFIKSPFTIICLVVDLAPSKGTVNLWTSRAGSKPVNHSRKEEKQKNG 404
QY 190 TLTVSTLPGTRDWEGETYQCRVTHPHLPALMRSTTKLPKRLAPEVYMLPPSPPEET 249
Db 405 TLTVSTLPGTRDWEGETYQCRVTHPHLPALMRSTTKLPKRLAPEVYMLPPSPPEET 464
QY 250 GTTRVTCLIRGFYSEISVQWLFNNEEDHTGHTTTTRPKDGHGTDPSFFLYSRMLVNKS 309
Db 465 GTTRVTCLIRGFYSEISVQWLFNNEEDHTGHTTTTRPKDGHGTDPSFFLYSRMLVNKS 524
QY 310 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342
Db 525 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 557

RESULT 15

US-10-453-915-18
; Sequence 18, Application US/10453915
; Publication No. US20040054146A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; APPLICANT: Persson, Stefan
; APPLICANT: Jansson, Asa
; TITLE OF INVENTION: Allergy Vaccines
; FILE REFERENCE: 10223-008001
; CURRENT APPLICATION NUMBER: US/10/453,915
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: 60/408,648
; PRIOR FILING DATE: 2002-09-05
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 566
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric polypeptide
US-10-453-915-18

Query Match 95.5%; Score 1772; DB 15; Length 566;
Best Local Similarity 98.5%; Pred. No. 1.4e-132;

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Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 10 LSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTVLVDGQEAEN 69
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
225 IDIPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTVLVDGQEAEN 284
QY 70 LFFYTRPRKREGGQTFSLQSEVNITOGQWSSNTYTCHVKHNGSIFEDSSRKCADSNPRG 129
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
285 LFFYTRPRKREGGQTFSLQSEVNITOGQWSSNTYTCHVKHNGSIFEDSSRKCADSNPRG 344
QY 130 VSAYLSRPSPPDLFIRKSPITITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQKNG 189
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
345 VSAYLSRPSPPDLFIRKSPITITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQKNG 404
QY 190 TLTVTSTLPVGTEDWIEGETYQCRVTHPHLPRALMRSTTKLPCKRLAPEVYMLPPSPPEET 249
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
405 TLTVTSTLPVGTEDWIEGETYQCRVTHPHLPRALMRSTTKLPCKRLAPEVYMLPPSPPEET 464
QY 250 GTTRTVTCLIRGYPSEISVQMLFNNEEDHTGHHITTRPKDGHGTDPPSFYSRMLVNKS 309
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
465 GTTRTVTCLIRGYPSEISVQMLFNNEEDHTGHHITTRPKDGHGTDPPSFYSRMLVNKS 524
QY 310 IMEXGNLVTCRVVHEALPGSRILEKSLHYSAGN 342
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
525 IMEXGNLVTCRVVHEALPGSRILEKSLHYSAGN 557
```

Search completed: November 14, 2004, 15:13:50
Job time : 145 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 14:55:22 ; Search time 40 Seconds
(without alignments)
822.653 Million cell updates/sec

Title: US-09-401-636-8
Perfect score: 1856
Sequence: 1 EFHHHHHTLSUPESGVTI.....HEALPGSRTLESLHYSAGN 342

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:**

- 1: P1r1:**
- 2: P1r2:**
- 3: P1r3:**
- 4: P1r4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1038.5	56.0	428	1 EHHU	Ig epsilon chain C
2	1024.5	55.2	426	2 I36548	Ig epsilon chain -
3	767.5	41.4	429	1 EHRT	Ig epsilon chain C
4	751.0	40.5	388	1 EHMS	Ig epsilon chain C
5	682.0	36.7	548	2 S38864	Ig epsilon chain C
6	673.0	36.3	423	1 EHMS	Ig epsilon chain C
7	580.5	31.3	572	2 B46529	Ig y heavy chain (
8	535.5	28.9	504	2 S00390	Ig mu chain C regi
9	497.5	26.8	479	1 MHREM	Ig mu chain C regi
10	496.0	26.7	454	1 MHRY	Ig mu chain C regi
11	495.5	26.7	458	1 MHRB	Ig mu chain C regi
12	486.5	26.2	326	1 G2HU	Ig gamma-2 chain C
13	480.5	25.9	343	2 S25644	Ig mu chain C regi
14	476.0	25.6	327	1 G4HU	Ig gamma-4 chain C
15	475.5	25.6	627	2 S14683	Ig mu chain precur
16	473.5	25.5	328	2 I47161	Ig gamma 3 chain -
17	472.0	25.4	433	2 S31436	Ig upsilon chain -
18	469.0	25.3	455	1 MHMS	Ig mu chain C regi
19	469.0	25.3	455	2 A24976	Ig mu chain C regi
20	469.0	25.3	476	1 MHMS	Ig mu chain C regi
21	468.0	25.2	328	2 I47160	Ig gamma 2b chain
22	465.0	25.1	328	2 I47159	Ig gamma 2a chain
23	465.0	25.1	453	2 S37768	Ig mu chain C regi
24	465.0	25.1	474	2 S15590	Ig heavy chain - h
25	463.5	25.0	328	2 I47158	Ig gamma 1 chain c
26	460.0	24.8	391	1 MHUHT	Ig mu heavy chain
27	458.5	24.7	592	2 S25705	Ig mu chain - shee
28	454.0	24.5	330	1 GHU	Ig gamma-1 chain C
29	453.5	24.4	452	1 MHU	Ig mu chain C regi

ALIGNMENTS

RESULT 1

BHHU

Ig epsilon chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004

C:Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02436; A53116; C4
R:Flanagan, J.G.; Rabbitts, T.H.

EMBO J. 1, 655-660, 1982

A:Title: The sequence of a human immunoglobulin epsilon heavy chain constant region gen

A:Reference number: A22771; MUID:84236029; PMID:6234164

A:Accession: A22771

A:Molecule type: DNA

A:Residues: 1-428 <FLA>

A:Cross-references: UNIPROT:P01854; GB:L00022; GB:J00227; GB:V00555; NID:G185035

R:Ueda, S.; Nakai, S.; Nishida, Y.; Hisajima, H.; Honjo, T.

EMBO J. 1, 1539-1544, 1982

A:Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudo

A:Reference number: A23195; MUID:84207910; PMID:6327276

A:Accession: A23195

A:Molecule type: DNA

A:Residues: 2-428 <UED>

A:Cross-references: GB:J00222; NID:G184755

R:Zhang, K.; Saxon, A.; Max, E.E.

J. Exp. Med. 176, 233-243, 1992

A:Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicin

A:Reference number: PH1214; MUID:92308839; PMID:1613458

A:Accession: PH1214

A:Molecule type: DNA

A:Residues: 320-428 <ZHA>

A:Cross-references: EMBL:X63693; GB:S38668; NID:G32987

R:Seno, M.; Kurokawa, T.; Ono, Y.; Onda, H.; Sasada, R.; Igarashi, K.; Kikuchi, M.; Sug

Nucleic Acids Res. 11, 719-726, 1993

A:Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon ch

A:Reference number: A93491; MUID:83168897; PMID:6300763

A:Accession: A93491

A:Molecule type: mRNA

A:Residues: 1-428 <SEN>

A:Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:G185035

R:Max, E.E.; Battay, J.; Ney, R.; Kirsch, I.R.; Leder, P.

Cell 29, 691-699, 1982

A:Title: Duplication and deletion in the human immunoglobulin epsilon genes.

A:Reference number: A90824; MUID:83001945; PMID:6288268

A:Accession: A90824

A:Molecule type: DNA

A:Residues: 1-358, 'L', 360-428 <MAX>

A:Cross-references: GB:J00222; NID:G184755

A:Note: this sequence difference may be due to polymorphism

R:Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.

in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-

A:Reference number: A94418

A:Accession: A94418

A:Molecule type: protein

Query Match 56.0%; Score 1038.5; DB 1; Length 428;
Best Local Similarity 62.4%; Pred. No. 7.7e-70;

Db 405 AVHEAASPSQTVORTVSVNPG 425

RESULT 3

EHRT

Ig epsilon chain C region - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 17-Dec-1992 #sequence_revision 17-Dec-1982 #text_change 09-Jul-2004
C:Accession: A93442; A90937; A02143
R:Hellman, L.; Pettersson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.
Nucleic Acids Res. 10, 6041-6049, 1992
A:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
A:Title: Structure and evolution of the heavy chain from rat immunoglobulin E.
A:Reference number: A93442; MUID:83064537; PMID:6292865
A:Accession: A93442
A:Molecule type: mRNA
A:Residues: 1-429 <HEL>
A:Cross-references: UNIPROT:P01855
A:Experimental source: strain LOU/c/Wsl, immunocytoma IR2
R:Kindsvogel, W.R.; Reddy, E.P.; Moore, J.M.; Faust Jr., C.H.
DNA 1, 335-343, 1982
A:Title: A cloned cDNA probe for rat immunoglobulin epsilon chain: construction, i
A:Reference number: A90937; MUID:83182019; PMID:6820340
A:Contents: myeloma IR162
A:Accession: A90937
A:Molecule type: mRNA
A:Residues: 'N', 169-307, 'L', 309-342 <KIN>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:19-80/Domain: immunoglobulin homology <IM1>
F:118-186/Domain: immunoglobulin homology <IM2>
F:223-291/Domain: immunoglobulin homology <IM3>
F:327-398/Domain: immunoglobulin homology <IM4>
F:45,99,170,240,265,369,419/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match 41.4%; Score 767.5; DB 1; Length 429;
Best Local Similarity 45.8%; Pred. No. 1.1e-49;
Matches 151; Conservative 54; Mismatches 114; Indels 11; Gaps 4;
QY 17 PVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFPAKVHTWLVGDGEAENLPYTR 76
Db PVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFPAKVHTWLVGDGEAENLPYTR 76
QY 77 PK---REGGQTFSLQSEVNTIQGWSNNTYTCVHKNHSIPEDSSRKCADSNPRGUSA 132
Db AQNVLKEGKLASTYSLRNITQQQWSBSTFCKVTSQGENYWAHTRCSDDEPRGVIT 210
QY 133 YLSRPFDFPIKSPFTITCLVVDLAPSKGTWNLTSRAGKPVNHSRKEKQKQNGTLT 192
Db YLIPPSFLDYENGTEPKLTCLVLDL-ESSENITVTVWRERKKSIGSASQSRKTHNATTS 269
QY 193 VTSTLPVGRDWTGEGTYQCRVTHPLPRALVRSTTKLPKGLAPRVNMLPPSPETGTT 252
Db ITSILPVADKNLEGYQCRVDHPFPPIVRSITAKFGKSAPVYVFLPPEEEKDK 329
QY 253 RVTCTIIRGYPSEISVQWLFNNEEDHTGHTTTRPQKHGTDPSFPFLSRMLVNKSIWE 312
Db RTLTCLIQNFPPEDISVQWLDKLPKSGHSTTTLKYNQSGNRRFFISRLVTKALWT 389
QY 313 KGNLVTCRVVHEALPGSRITLKSLSHYSAGN 342
Db QTQKTCRVVHEALPRKLTITSKSLGN 419

RESULT 4

EHNS

Ig epsilon chain C region (version 1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
C:Accession: A02144
R:Liou, F.T.; Albrandt, K.; Sutcliffe, J.G.; Katz, D.H.
Proc. Natl. Acad. Sci. U.S.A. 79, 7852-7856, 1982

A:Title: Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA.
A:Reference number: A02144; MUID:83117774; PMID:6818553
A:Accession: A02144
A:Molecule type: mRNA
A:Residues: 1-388 <LIU>
A:Cross-references: UNIPROT:P06336; GB:J00476; NID:g194875; PIDN:AAA38085.1; PID:g38722
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:1-44/Domain: immunoglobulin homology (fragment) <IM1>
F:81-149/Domain: immunoglobulin homology <IM2>
F:186-254/Domain: immunoglobulin homology <IM3>
F:290-361/Domain: immunoglobulin homology <IM4>
F:10,51,62,133,205,228,332,382/Binding site: carbohydrate (Asn) (covalent) #status pred

Query Match 40.5%; Score 751; DB 1; Length 388;
Best Local Similarity 44.8%; Pred. No. 1.7e-48;
Matches 155; Conservative 53; Mismatches 130; Indels 8; Gaps 4;
QY 2 FHHHHHTLSLPES-----GPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFPAKV 56
Db FTCHVTHPPSPFNESRTILVRPNVITEPTLELLHSSCDPNA-FHSTIQLCYCFIYGHILNDV 98
QY 57 HVTWLVGDGEAENLPYTRPRKGGQTFSLQSEVNTIQGWSNNTYTCVHKNHSIFE 116
Db SVSLMDDREITDLAQVLIKEE-GKLASTCCKNITEQQWSESTFTCKVTSQGVLY 157
QY 117 DSSRKCADSNPRGVSAYLSRSPDFPIKSPFTITCLVVDLAPSKGTWNLTSRAGKPV 176
Db ATRRCDPDHPRGVITYLIPSPDLQYQNGAPKLTCLVVDLESEK-NVNVTWNOEKKTSV 216
QY 177 NHRTRKEKQKQNGTLTSTLPVGRDWTGEGTYQCRVTHPLPRALVRSTTKLPKGLA 236
Db SASQWYTKHNNATTSITSLPVVAKOWIEGYQCVVDHPDFKPIVRSITKTPGQRSA 276
QY 237 PEVYMLPPSPETGTTTRVTCILRGYPSEISVQWLFNNEEDHTGHTTTRPQKHGTD 296
Db PEVYVFPPEBESEDKRTLTCLIQNFPPEDISVQWLDGKLSNSQHSSTTTPKLSNSNQ 336
QY 297 SFYYSRMLVNKSIWEKGNLVTCRVVHEALPGSRITLKSLSHYSAGN 342
Db GFFIFSRLEVAKLTWTKQTCQVIHEALQKPRKLEKTISTSLGN 382

RESULT 5

S38864

Ig epsilon chain C region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001
C:Accession: S38864
R:Kipp, B.; Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A:Description: Combination of a defined specificity and desired isotype by cloning of a
A:Reference number: S38864
A:Accession: S38864
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-548 <KIP>
A:Cross-references: EMBL:Z27397; NID:g416537; PIDN:CAA81788.1; PID:g940782
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:353-421/Domain: immunoglobulin homology <IMV>

Query Match 36.7%; Score 682; DB 2; Length 548;
Best Local Similarity 43.0%; Pred. No. 3.6e-43;
Matches 142; Conservative 52; Mismatches 122; Indels 14; Gaps 4;

QY 12 LPESGPVTIIPPTVKLFHSSCDPRGD--AHSTIQLCLVSGFPAKVHTWLVGDQAEEN 69
Db VPEVSSVFIFPKPK-----DVLTRSTIQLCYCFIYGHILNDVSVSLMDDREITD 278
QY 70 LPYVTRPRKGGQTFSLQSEVNTIQGWSNNTYTCVHKNHSIFEEDSSRKCADSNPRG 129

Db 279 TLAQTVLKEE-GKLASTCKLNITEQOWNSESTFTCKVTSGVDYLAHTRCPDHEPRG 337
 QY 130 VSAIYLRSPDFLPIKSTITCLVVDLAPSGTGNLTWSRAGKPVNHSIRKEKQNG 189
 Db 338 VITYLIPSPDLQYNGAPKLTCLVVDLESEK-VNVTWNQSKTSVSAQWYTKHNA 396
 QY 190 TLVTITLPLVGTDMTEGYTCQVTHPLPALMRSTTKLPKRLAPEVYMLPSPSET 249
 Db 397 TTSITSLPVAKDWIEGYGYCIVDHPDFPKPIVRSITKTQGSASEVYVFPPEES 456
 QY 250 GTTRVTCLIRGYPSEISVQWLFNNEEDHTGHTTTRQKHGTDPSFFLYSRMLVNS 309
 Db 457 EDKRTLTCLIQNFPPDISVQWLDGKLINSQHSHTTTLKSGNSNRGFFIPSRLEAVT 516
 QY 310 IWEKGNLVTCTRVVHEALPGSRTLEKSLHYS 339
 Db 517 LWTQKQFTQCVTHEALQPKRLEKTIIST 546

RESULT 6
 ERMSS
 Ig epsilon chain C region (version 2) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
 C:Accession: A02145
 R:Ushida, N.; Ueda, S.; Hayashida, H.; Miyata, T.; Honjo, T.
 EMBO J. 1, 1117-1123, 1982
 A:Title: The nucleotide sequence of the mouse immunoglobulin epsilon gene: comparison with human epsilon gene
 A:Reference number: A90966; MUID:84236092; PMID:6329728
 A:Accession: A02145
 A:Molecule type: DNA
 A:Residues: 1-423 <ISH>
 A:Cross-references: UNIPROT:P06336
 A:Note: the sequence was determined from the germline gene
 C:Genetics:
 A:Introns: 91/1; 199/1; 307/1
 A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F:16-77/Domain: immunoglobulin homology <IMM1>
 F:115-183/Domain: immunoglobulin homology <IMM2>
 F:220-288/Domain: immunoglobulin homology <IMM3>
 F:325-396/Domain: immunoglobulin homology <IMM4>
 F:23-75,122-181,227-286,332-394/disulfide bonds: #status predicted
 F:43,84,167,239,262,417/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 36.3%; Score 673; DB 1; Length 423;
 Best Local Similarity 41.6%; Pred. No. 1.2e-42;
 Matches 147; Conservative 53; Mismatches 133; Indels 20; Gaps 7;

QY 2 FHHHHHTLSPSGVPTIIPVTKLFS-----SCDPRGDAHSTIQLCLVSGF 51
 Db 73 FTCHVTHPPSFNSRITLVRPVT---HSLSPWMSIHRCPDFA-FHSTIOLYCFIYGH 127
 QY 52 SPAKVHTVMDVQEAENLPFYTRPKRGQTFSLQSEVNITQGMWSSNTYTCVHXNH 111
 Db 128 ILNDVSVWMLDDREITDLAQTVLKEE-GKLASTCKLNITEQOWNSESTFTCRVTSQ 186
 QY 112 GSIFEDSSRKACDNRPGVSAIYLRSPDFLPIKSTITCLVVDLAPSGTGNLTWSR 171
 Db 187 GVDYLAHTRCPDHEPRGAIITLIPSPDLQYNGAPKLTCLVVDLESEK-VNVTWNQ 245
 QY 172 SGKPVNHSIRKEKQNGTLTSTVPGTRDWIEGYTCQVTHPLPALMRSTTKLP 231
 Db 246 KTSVSAQWYTKHNNATISITSLPVAKDWIEGYGYCIVDHPDFPKPIVRSIT 304
 QY 232 --GKRLAPEVYMLPSPSETGTTTTCVCLIRGYPSEISVQWLFNNEEDHTGHTTTRPQ 289
 Db 305 QVSGRAPEVYVFPPEESSEDKRTLTCLIQNFPPDISVQWLDGDKLINSQHSHTTTL 364
 QY 290 KDHGTDPSFFLYSRMLVNSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342

Db 365 KSGNSQGFIFSRLEAVKTLWTQKQFTQCVTHEALQPKRLEKTIISTSLGN 417

RESULT 7
 B46529
 Ig Y heavy chain (7.8S) - duck
 N:Alternate names: Ig gamma chain (7.8S)
 C:Species: Anas platyrhynchos (domestic duck)
 C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
 C:Accession: B46529; S20759
 R:Magor, K.E.; Warr, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.
 J. Immunol. 149, 2627-2633, 1992
 A:Title: Structural relationship between the two Igy of the duck, Anas platyrhynchos: molecular cloning and sequencing of the heavy chain genes
 A:Reference number: A46529; MUID:93017865; PMID:1401901
 A:Accession: B46529
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-572 <MAG>
 A:Cross-references: EMBL:X65219; NID:962442; PIDN:CAA46322.1; PID:962443
 A:Experimental source: spleen
 A:Note: sequence extracted from NCBI backbone (NCBIP:116127)
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:37-120/Domain: immunoglobulin homology <IMM>

Query Match 31.3%; Score 580.5; DB 2; Length 572;
 Best Local Similarity 38.2%; Pred. No. 1.4e-35;
 Matches 124; Conservative 56; Mismatches 130; Indels 15; Gaps 9;

QY 22 PPTVKLPHSS-CDPRGDAHSTIQLCLVSGFSPAKVHTVMDVQEAENLPFYTRPKRE 80
 Db 249 PPEVQLHSSVCSTLGD--DSVELLCVITGFSPPVEVWLVGDGAP-HLVATWTRPQRE 305
 QY 81 -GGQTFSLQSEVNITQGMWSSNTYTCVHXH--NGSIFEDSSRKACDNRPG--VSAVL 134
 Db 306 AGSKTYMATSTQNVSRDWDKAGKAFTRVKKHPATGTAQGHAFRCFSGAQCSPQIFV 365
 QY 135 SRSPDFLPIKSTITCLVVDLAPSGTGNLTWSRAGKPVNHSIRKEKQNGTLT 194
 Db 366 VPSPGLYLRQAKVHCLVNL-PSDASLSISWTREKSGALRPDPMLVTEHNGFTTAS 424
 QY 195 STLFPVGTDRWIEGYTCQVTHPLPALMRSTTKLPKRLAPEVYMLPSPSETGTTT 253
 Db 425 SSLAISTQDMLAGERFTCTVQHEDLPVPLGKSLAKIAGKVTAIYTFPPHABELSLAEV 484
 QY 254 TVTCLIRGFPSPISVQWLFNNEEDHTGHTTTRQKHGTDPSFFLYSRMLVNSIWEK 313
 Db 485 TLCTLRGQFQPEHVEVQWLNHNHNSVPAAEFVTPPLKEPNQDGTFFLYSKMTVPKASWQ 544
 QY 314 GNLVTCRVVHEALP--GSRTLEKS 335
 Db 545 GVSACVWVHEGLPMRFTQEPLOKT 569

RESULT 8
 S00390
 Ig gamma chain (clone 36) - chicken (fragment)
 N:Alternate names: Ig nu chain
 C:Species: Gallus gallus (chicken)
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jan-2000
 C:Accession: S00390
 R:Parvari, R.; Avivi, A.; Lentner, F.; Ziv, E.; Tel-Or, S.; Burstein, Y.; Schechter, I.
 EMBO J. 7, 739-744, 1988
 A:Title: Chicken immunoglobulin gamma-heavy chains: limited VH gene repertoire, combination of D and J segments, and the role of the C region in the formation of the heavy chain
 A:Reference number: S00390; MUID:88283642; PMID:3135182
 A:Accession: S00390
 A:Molecule type: mRNA
 A:Residues: 1-504 <PAR>
 A:Cross-references: EMBL:X07174
 A:Note: this sequence was determined from the differentiated gene
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin


```
Db 389 APLHYTHSVLTVTEBWSNGETTCVVGHEALPHMVTERTVDRS 433
RESULT 11
MHRB
Ig mu chain C region, secreted form - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 09-Jul-2004
C:Accession: A02164
J:Bernstein, K.E.; Alexander, C.B.; Reddy, E.P.; Mage, R.G.
J:Immunol. 132, 490-495, 1984
A:Title: Complete sequence of a cloned cDNA encoding rabbit secreted mu-chain of V-Ha2 a
A:Reference number: A02164; MUID:84088930; PMID:6418803
A:Contents: a2 allotype
A:Accession: A02164
A:Molecule type: mRNA
A:Residues: 1-458 <BER>
A:Cross-references: UNIPROT:P03988
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu
F:21-32/Domain: immunoglobulin homology <IMM1>
F:130-202/Domain: immunoglobulin homology <IMM2>
F:242-310/Domain: immunoglobulin homology <IMM3>
F:349-420/Domain: immunoglobulin homology <IMM4>
F:14/Disulfide bonds: interchain (to light chain) #status predicted
F:28-90,137-200,308,356-418/Disulfide bonds: #status predicted
F:46,114,212,261,277,284,445/Binding site: carbohydrate (Asn) (covalent) #status predict
F:219,457/Disulfide bonds: interchain (to heavy chain) #status predicted
F:236/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted
Query Match 26.7%; Score 495.5; DB 1; Length 458;
Best Local Similarity 33.1%; Pred. No. 2.2e-29;
Matches 116; Conservative 61; Mismatches 148; Indels 25; Gaps 10;
QY 5 HHHTLSLPESGV-TIIPYVKLPHSSCDPR----GDAHSITQLLCVSGSPAKVHT 59
Db 94 HNSNDRLVSPFVDSLPVSFV---IPPRDSFGSGTRKSLRICATGSPKQISVS 150
QY 60 WLVDGQAEAN---LFPYTRPRKREGQTESLQSEVNIQGWSSNTVTCHVKNHSIFE 116
Db 151 WLVDGQKVESGLTKPVEATKAGPATFSISMLTIESDWLSQSLYTCRVDHRGIFD 210
QY 117 DS---SRKCADSNPRGVAYLSRPFDFPIKSPPTICLVVDLAPSGKTNLWTSRAG 173
Db 211 KVMSESECTTPSPGIQVFPFAPSPADTFLSKARLICLVTDLT-TYGSLSNWSHNG 269
QY 174 KPVNHSTRKEKORNTLTVTSLPVGTRDWIEGETYQCRVTHPHLPALMRSTTKLPKG 233
Db 270 KALDTHMNTESHNPATFAMEASVCAEDWSGQFCTVTHADLPFLKHTISK--SR 327
QY 234 RLA---PEVYMLPPSPPEE--TGTRVTCCLIRGFVPSSEISVQWLFNNEEDTGHHTTRP 288
Db 328 EVAKHPVAVVYLPAPAEQLVRESATVTCVXGFSFADVFVQVQVQVQVQVQVQVQV 387
QY 289 QKDHGTDTPFFLYSLVKNKSTWEKGNLVCRTVWHEALP---GSRLEKS 335
Db 388 APEQAPQAGLYFTHSTLTVTTEEDWNSGETTTCVVGHEALPHMVTERTVDRS 437
RESULT 12
G2HU
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence_revision 13-Jun-1993 #text_change 09-Jul-2004
C:Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A:Title: Linkage and sequence homology of two human immunoglobulin gamma chain con
A:Reference number: A93906; MUID:82197621; PMID:6804948
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:932759; PIDN:CAB58438.1; P
A:Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J:Immunol. 125, 1048-1054, 1980
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A:Reference number: A92809; MUID:81007873; PMID:6774012
A:Contents: myeloma protein Til
A:Accession: A92809
A:Molecule type: protein
A:Residues: 1-19, Q, 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A:Note: Trp-156 is at or near the complement-binding site
R:Connell, G.B.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of a
A:Reference number: A90752; MUID:80001357; PMID:113060
A:Contents: myeloma protein Zie
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
A:Note: this sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A:Reference number: A93132; MUID:80114419; PMID:118920
A:Contents: Zie
A:Accession: A93132
A:Molecule type: protein
A:Residues: 238-275 <HOF>
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas. March 1980
A:Reference number: A94591
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidati
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500; PMID:4940472
A:Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124; PMID:5782707
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:133-202/Domain: immunoglobulin homology <IM2>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,140-200,246-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:116/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 26.2%; Score 486.5; DB 1; Length 326;
Best Local Similarity 36.2%; Pred. No. 6.7e-29;
Matches 117; Conservative 57; Mismatches 120; Indels 29; Gaps 11;
QY 35 RGAHSITQLLCVSGSPAKVHTW---LVVDGQAEANLFPYTRPRKREGQTFSLQSE 90
Db 16 RSTSESTAALGCVLKQVDFPEFVTVSNWSGALTSG---VHTFPAVL-----QSSGLYSLSSV 68
QY 91 VNITQGWSSNTYTCVHKH---NGSIFEDSSRKCADSNP-----RGVSAYLSRSPSF 140
Db 69 VTPSSNF-GTQYTCNVNDHKPSNTKVDKVERKCCVCCPAPVAGSPVFLFPKPK 127
```

QY 141 D-LFIRKSPITICLVVDLAPSKGTNLVTSRASGKPVNHSRKEEKQKORNGTLTSTLPV 199
Db 128 DTLMIKRTPEVTCVVDVSHEDDEVQFNVDVGVHNAKTRPEQFNSTRFVSVLTV 187
QY 200 GTEDWIEGETYQCRVTHPHLPALMRSTTKLPGKRLAPEVYMLPPSPPEE-TGTRTVTC 258
Db 188 VHGDWLNKREYCKVKNKGLPADIEKTIKTKGQPREPQVYTLPPSREEMTKNQVSLTCL 247
QY 259 IRGFYFSEISVQWLFNNEEDHTGHTTTPQKDHGTDPSFFLYSRMLVKNKSIWEKGNLV 318
Db 248 VKGFYFSDIAVESNGQPEN--NYKTPPMLD--SDGSFFLYSKLTVDKSRWQGNVPS 303
QY 319 CRVVEALPGSRTEKSLHYSG 341
Db 304 CSVMHEALNHHT-QKSLSLSPG 325

RESULT 13
S25644
Ig mu chain C region - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 20-Feb-1995 #sequence_revision 30-Jan-1998 #text_change 21-Jan-2000
C/Accession: S25644
R/Parker, K.; Bugeon, L.; Soullou, J.P.
Submitted to the EMBL Data Library, September 1992
A/Reference number: S25644
A/Accession: S25644
A/Molecule type: mRNA
A/Residues: 1-343 <PAR>
A/Cross-references: EMBL:X68312; NID:G56461; PIDN:CAA48392.1; PID:G818025
A/Experimental source: spleen
C/Genetics:
A/Map position: 6
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: immunoglobulin
F:234-305/Domain: immunoglobulin homology <IMM>

Query Match 25.9%; Score 480.5; DB 2; Length 343;
Best Local Similarity 34.7%; Pred. No. 2e-28;
Matches 108; Conservative 59; Mismatches 131; Indels 13; Gaps 7;

QY 36 GDAHSTIQLCLVSGSPAKVHTVWLVDQEAENLF---PYTRPKREGQTFSLQSEVN 92
Db 14 GPAPRSRLICEATNESPQITVSWLQDGKPKVSGFTTEPVVEAKGSRPQYKVISLT 73
QY 93 ITGQWMSNTYCHVKNGSIF-EDSRKCADSNPRGVSAVLSRSPDLPFKSPIT 151
Db 74 ITESDWINLVFCRVDHRLGLTFWKNVSTCAASPSDILAPIPPSFADIFLTSAKL 133
QY 152 CLVVDLAPSKGTNLVTSRASGKPVNHSRKEEKQKORNGTLTSTLPVGTROWIEGETYQ 211
Db 134 CLVTNLA-TYDTLNISSWSKSGEPLTNTKIMESHNPNGTFSVAVGVASVCMEDWNRKGFV 192
QY 212 CRVTHPHLPALMRSTTKLPGK--RLAPEVYMLPPSPPEE--TGTRTVTCIRGYPSEI 267
Db 193 CTVTHRDLPSPQCKFISK-PNEVAKHPAPVAYLLPAREQLILRESATVCLVKGFSPADI 251
QY 268 SVQWLFNNEEDHTGHTTTPQKDHGTDPSFFLYSRMLVKNKSIWEKGNLVTCRVVHEALP 327
Db 252 FVQWLQGLSDSKVYTSAPWPEPCAPGLYTHSLTITVEEWSNGEYTCVVGHEALP 311

QY 328 ---GSRTLEKS 335
Db 312 HMVTERTVDKS 322

RESULT 14
G4HU
Ig gamma-4 chain C region - human
C/Species: Homo sapiens (man)
C/Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C/Accession: A90933; A90249; A02150
R/Ellison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981.
A/Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A/Reference number: A90933; MUID:83157104; PMID:6299662
A/Accession: A90933
A/Molecule type: DNA
A/Residues: 1-327 <ELL>
A/Cross-references: UNIPROT:P01861
A/Note: the sequence was determined from the germline gene
R/Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A/Title: Human immunoglobulin subclases. Partial amino acid sequence of the constant
A/Reference number: A90249; MUID:70207560; PMID:4192699
A/Accession: A90249
A/Molecule type: protein
A/Residues: 1-30; 81-326 <PIN>
C/Genetics:
A/Gene: GDB:IGHG4
A/Cross-references: GDB:119340; OMIM:147130
A/Map position: 1q32.33-1q32.33
A/Introns: 99/1; 111/1; 221/1
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:99-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83, 141-201, 247-305/Disulfide bonds: #status predicted
F:106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 25.6%; Score 476; DB 1; Length 327;
Best Local Similarity 35.8%; Pred. No. 4.1e-28;
Matches 116; Conservative 57; Mismatches 121; Indels 30; Gaps 10;

QY 35 RGDHSTIQLCLVSGSPAKVHTVWL---LVQGEAENLFVYTRPKREGQTFSLQSE 90
Db 16 RSTSESTAALGCLVKYDFPEPVTVMNSGALTSG---VHTFPAVL---QSSGLYSLSV 68
QY 91 VNITQGMWSSNTYCHVKNGSIFEDSRKCADSNP-----RGVSAYLSRPPSP 139
Db 69 VTFVSS--LGKTYTCNVVDHKPSNTKVDKVESKYGPCPCAPAEFLGGPSVFLPPKP 127
QY 140 FD-LFIRKSPITICLVVDLAPSKGTNLVTSRASGKPVNHSRKEEKQKORNGTLTSTLP 198
Db 128 KDTLMISRTPEVTCVVDVSHEDDEVQFNVDVGVHNAKTRPEQFNSTRFVSVLTV 187
QY 199 VGTEDWIEGETYQCRVTHPHLPALMRSTTKLPGKRLAPEVYMLPPSPPEE-TGTRTVTC 257
Db 188 VLHQDLNKGREYCKVKNKGLPSSIEKTIKSKAGQPREPQVYTLPPSREEMTKNQVSLT 247
QY 258 LIRGFYFSEISVQWLFNNEEDHTGHTTTPQKDHGTDPSFFLYSRMLVKNKSIWEKGNLV 317
Db 248 LVKGFYFSDIAVESNGQPEN--NYKTPPVLDD--SDGSFFLYSLTVDKSRWQGNV 303
QY 318 TCRVVEALPGSRTEKSLHYSG 341
Db 304 CSVMHEALNHHT-QKSLSLSLG 326

RESULT 15
S14683
Ig mu chain precursor, membrane-bound (clone 201) - human
C/Species: Homo sapiens (man)
C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C/Accession: S14683; S08047
R/Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A/Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain
A/Reference number: S14683; MUID:90332450; PMID:2115996
A/Accession: S14683

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OM protein - protein search, using sw model

Run on: November 14, 2004, 14:55:18 ; Search time 191 Seconds
(without alignments)
1030.252 Million cell updates/sec

Title: US-09-401-636-8
Perfect score: 1856
Sequence: 1 EFHHHHHTLSLPESGPTI.....HEALPGSRTLESLHYSAGN 342

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 02: *
1: uniprot_prot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1038.5	55.0	428	1 EPC HUMAN	P01854 homo sapien
2	1033.5	55.7	571	2 BAC85440	Bac85440 homo sapi
3	767.5	41.4	429	1 EPC RAT	P01855 rattus norv
4	751	40.5	421	1 EPC_MOUSE	P06336 mus musculu
5	497.5	26.8	479	1 MUCM_RABIT	P04221 oryctolagus
6	496.5	26.8	464	2 Q6MZU6	Q6mzu6 homo sapien
7	496.5	26.8	464	2 CAE45931	CAe45931 homo sapi
8	495.5	26.7	458	1 MUC_RABIT	P03988 oryctolagus
9	493.5	26.6	464	2 BAC85395	Bac85395 homo sapi
10	493.5	26.6	468	2 BAC85483	Bac85483 homo sapi
11	488.5	26.3	465	2 Q6PEC4	Q6pec4 homo sapien
12	488.5	26.3	465	2 AAH62335	AAh62335 homo sapi
13	486.5	26.2	326	1 GC2 HUMAN	P01859 homo sapien
14	486.5	26.2	417	2 Q6N093	Q6n093 homo sapien
15	486.5	26.2	417	2 CAE45777	CAe45777 homo sapi
16	483	26.0	454	1 MUC_MSAU	P06337 mesocricetu
17	482.5	26.0	337	2 Q95W34	Q95w34 equus cabal
18	482.5	26.0	472	2 BAC85393	Bac85393 homo sapi
19	479.5	25.8	473	2 Q8TC63	Q8tc63 homo sapien
20	479.5	25.8	476	2 Q6MXZ7	Q6mxz7 homo sapien
21	479.5	25.8	476	2 CAE45900	CAe45900 homo sapi
22	476	25.6	327	1 GC4 HUMAN	P01861 homo sapien
23	475.5	25.6	454	1 MUC_HUMAN	P01871 homo sapien
24	470	25.3	614	2 Q7MT5	Q7mt5 mus musculu
25	469	25.3	455	1 MUC_MOUSE	P01872 mus musculu
26	468	25.3	476	1 MUCM_MOUSE	P01873 mus musculu
27	469	25.3	613	2 Q8VCX7	Q8vcx7 mus musculu
28	467	25.2	548	2 BAD00196	Bad00196 camelus d
29	465	25.1	375	2 Q86T1	Q86t1 homo sapien
30	465	25.1	480	2 Q6PJF1	Q6pjf1 homo sapien
31	465	25.1	480	2 AAH16381	AAh16381 homo sapi

32 465 25.1 595 2 Q8WUX4 Q8wux4 homo sapien
33 465 25.1 597 2 Q8GMX5 Q8gmX5 homo sapien
34 465 25.1 597 2 Q8BQB8 Q8bqb8 homo sapien
35 465 25.1 597 2 Q9BU10 Q9bul0 homo sapien
36 465 25.1 597 2 Q9BB9 Q9bb9 homo sapien
37 465 25.1 606 2 Q6GMX2 Q6gmy2 homo sapien
38 465 25.1 613 2 Q8WUX1 Q8wuk1 homo sapien
39 465 25.1 620 2 Q9EYO Q9eey0 homo sapien
40 465 25.1 625 2 Q96AA6 Q96aa6 homo sapien
41 462 24.9 470 2 BAC85387 Bac85387 homo sapi
42 462 24.9 479 2 AAH14667 AAh14667 homo sapi
43 460 24.8 391 1 MUCB_HUMAN P04220 homo sapien
44 460 24.8 483 2 BAC85202 Bac85202 homo sapi
45 459.5 24.8 477 2 BAC85697 Bac85697 homo sapi

ALIGNMENTS

RESULT 1
EPC_HUMAN STANDARD; PRT; 428 AA.
AC P01854;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE IG epsilon chain C region.
GN Name=IGHE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83168897; PubMed=6300763;
RA Seno M., Kurokawa T., Ono Y., Okada H., Sasada R., Igarashi K.,
RA Kikuchi M., Sugino Y., Nishida Y., Honjo I.;
RT "Molecular cloning and nucleotide sequencing of human immunoglobulin
RT epsilon chain cDNA.";
RL Nucleic Acids Res. 11:719-726 (1983).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT LEU-359.
RX MEDLINE=83001945; PubMed=6289268;
RA Max E.E., Battey J., Key R., Kirsch I.R., Leder P.;
RT "Duplication and deletion in the human immunoglobulin epsilon genes.";
RL Cell 29:691-699 (1982).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=84236029; PubMed=6234164;
RA Flanagan J.G., Rabbits T.H.;
RT "The sequence of a human immunoglobulin epsilon heavy chain constant
RT region gene, and evidence for three non-allelic genes.";
RL EMBO J. 1:655-660 (1982).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=84207910; PubMed=6327276;
RA Ueda S., Nakai S., Nishida Y., Hisajima H., Honjo T.;
RT "Long terminal repeat-like elements flank a human immunoglobulin
RT epsilon pseudogene that lacks introns.";
RL EMBO J. 1:1539-1544 (1982).
RN [5]
RP PRELIMINARY SEQUENCE (MYELOMA PROTEIN ND).
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RT (In) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
RN [6]
RP SEQUENCE OF 1-40; 68-114 AND 427-428 FROM N.A.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.J.;
RT "Cloning and sequence determination of the gene for the human
RT immunoglobulin epsilon chain expressed in a myeloma cell line.";

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RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [7]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=87089848; PubMed=3796618;
RA Padlan E.A., Davies D.R.;
RT 'A model of the Fc of immunoglobulin E.';
RL Mol. Immunol. 23:1063-1075(1986).
CC -!- SIMILARITY: Contains 4 immunoglobulin-like domains.
CC -----
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CC -----
CC EMBL: L00022; AAB59424.1; ALT_INIT.
DR FIR; A22771; EHHU.
DR PDB; 1F6A; X-ray; B/D=207-428.
DR PDB; 1FP5; X-ray; A=207-428.
DR PDB; 1G84; NMR; A=106-210.
DR PDB; 1IG3; Model; A/B=-.
DR PDB; 1OOV; X-ray; A/B=102-428.
DR Genew; HGNC:5522; IGHE.
DR MIM; 147180; -.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00407; IGcl; 4.
DR PROSITE; PS00835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
DR 3D-structure; Direct protein sequencing; Glycoprotein;
KW Immunoglobulin C region; Immunoglobulin domain; Repeat.
FT NON_TER 1
FT DOMAIN 6 103 IG-like 1.
FT DOMAIN 112 210 IG-like 2.
FT DOMAIN 214 318 IG-like 3.
FT DOMAIN 324 423 IG-like 4.
FT DISULFID 14 14 Interchain (with a light chain).
FT DISULFID 15 105 Interchain (with a heavy chain).
FT DISULFID 29 85 Interchain (with a heavy chain).
FT DISULFID 121 121 Interchain (with a heavy chain).
FT DISULFID 135 193 Interchain (with a heavy chain).
FT DISULFID 209 299 N-linked (GlcNAc. . .).
FT DISULFID 239 299 N-linked (GlcNAc. . .).
FT DISULFID 345 405 N-linked (GlcNAc. . .).
FT CARBOHYD 21 21 N-linked (GlcNAc. . .).
FT CARBOHYD 49 49 N-linked (GlcNAc. . .).
FT CARBOHYD 99 99 N-linked (GlcNAc. . .).
FT CARBOHYD 146 146 N-linked (GlcNAc. . .).
FT CARBOHYD 252 252 N-linked (GlcNAc. . .).
FT CARBOHYD 275 275 W -> L (possible polymorphism).
FT VARIANT 359 359 /FTID=VAR_003885.
FT STRAND 113 119;
FT STRAND 130 138;
FT STRAND 148 151;
FT TURN 152 153;
FT STRAND 154 156;
FT STRAND 163 165;
FT STRAND 173 181;
FT STRAND 182 186;
FT TURN 187 188;
FT STRAND 191 196;
FT STRAND 201 206;
FT STRAND 218 221;
FT HELIX 226 230;
FT TURN 231 232;

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FT STRAND 236 244
FT TURN 252 257
FT STRAND 258 259
FT STRAND 267 272
FT TURN 274 275
FT STRAND 278 285
FT HELIX 288 292
FT TURN 293 294
FT STRAND 297 302
FT TURN 304 305
FT STRAND 310 314
FT STRAND 322 322
FT STRAND 325 330
FT STRAND 334 334
FT STRAND 335 336
FT TURN 337 337
FT STRAND 340 351
FT STRAND 356 361
FT TURN 362 363
FT STRAND 364 365
FT HELIX 368 370
FT STRAND 371 373
FT STRAND 377 378
FT STRAND 384 393
FT HELIX 394 399
FT STRAND 403 408
FT TURN 410 411
FT TURN 413 415
FT STRAND 417 422
SQ SSEQUENCE 428 AA; 25CA072AAS58A0 CRC64;

Query Match 56.0%; Score 1038.5; DB 1; Length 428;
Best Local Similarity 62.4%; Pred. No. 9.3e-72;
Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;

Qy 22 PPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTVWLVDGQEAENLFPVTTREKRG 81
Db 111 PPTVKILQSSCDGGHFPPTIQLCLVSGFTPTQITWLEDCQVND--VDLSTASTTQE 168
Qy 82 GQTFSLQSEVNIITQGMMSNTYTCHVXNGSIFEDSRKCADSNPRGVSAYLSRSPFD 141
Db 169 GELASTQSELTLSQKEWLSDRYTCQTYQGTFEDSTKKCADSNPRGVSAYLSRSPFD 228
Qy 142 LFRKSPPTITCLVVDLAPSGKTNLWSRAGSPVNHSTRKEKQKNGTLTSTLPVGT 201
Db 229 LFRKSPPTITCLVVDLAPSGKTNLWSRAGSPVNHSTRKEKQKNGTLTSTLPVGT 288
Qy 202 RDMIEGTQYQCRVTHPLPALMRSTTKLPKRLAPEVIMLPPSPETGT--TRTVTCLI 259
Db 289 RDMIEGTQYQCRVTHPLPALMRSTTKTSGPRAAPEVYAF-ATPEWPGSRDKRTLACLI 347
Qy 260 RGFYPSISVQWMLFNNEEDHTGHTTTRPOKHGTDPSPFLYSRMLVNSIKWKNLVC 319
Db 348 QNFMPEDISVQWMLHNEVQLPDARHSTTPRKTGKS--GPEVFSRLVETRAEWKQDEFC 405
Qy 320 RVVHEALPGSRTLEKSLHYSAG 341
Db 406 RAVEHAASPSQTQVRAVSNVPG 427

RESULT 2
BAC85440 PRELIMINARY; PRT; 571 AA.
ID BAC85440
AC BAC85440; (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE CDNA FLJ27315 fis, clone TMS06851, highly similar to Ig epsilon chain
DE C region.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;

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RN SEQUENCE FROM N.A.
RP TISSUE=Thymus;
RA Nakagami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T.,
RA Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK130825; BAC8540.1; -.
SQ SEQUENCE 571 AA; 62602 MW; E920D06277B8D2FF CRC64;

Query Match 55.7%; Score 1033.5; DB 2; Length 571;
Best Local Similarity 61.9%; Pred. No. 3.2e-71; Indels 13; Gaps 7;
Matches 205; Conservative 41; Mismatches 72;

QY 15 SGVPTIIPVTKLFHSCDPRGDAH--STIQLCLVSGFSPAKVHVTLVLDQAEANLFP 72
Db 249 SGDFT--PPTVKILQSCD--GGEHFPPTIQLCLVSGVTPGTGTTNITWLEDQVMD--VD 302
QY 73 YTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSRKCADSNRGVSA 132
Db 303 LSTASTQGEHLASTQSELTLSQKWLSDRTYTCQVYQGHFTFEDSTKCADSNRGVSA 362
QY 133 YLSRSPFDLFIKRSPTITCLVVDLAPSKGTNLTWSRAGKPVNHSRKEEKQKNGILT 192
Db 363 YLSRSPFDLFIKRSPTITCLVVDLAPSKGTNLTWSRAGKPVNHSRKEEKQKNGILT 422
QY 193 VTSLPVGTRDWIEGETYQCRVTHPHLPALMRSTTKLPGLKLAPEVYVMLPPSEETGTT 251
Db 423 VTSLPVGTRDWIEGETYQCRVTHPHLPALMRSTTKLPGLKLAPEVYVMLPPSEETGTT 481
QY 252 -TRTVCLIRGFYPSISVQWLFNNEEDHTGHHTTTRPKQDGTDPSPFLYSRMLVYKSI 310
Db 482 DKXTLACLQNFPEDISVQWLHNEVQLPDARHSTTQPKTKGS--GFFVFSRLVETRAE 539
QY 311 WEKGNLVTRCVVHEALPGSRTEKSLHYSA 341
Db 540 WEQKEFICRAVHAASPSQTVQRAVSNVPG 570

RESULT 3
EPC_RAT ID EPC_RAT STANDARD; PRT; 429 AA.
AC P01855;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig epsilon chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (IMMUNOCYTOMA IR2).
RC STRAIN=LOU/C/WSU;
RX MEDLINE=83064537; PubMed=6292865;
RA Hellman L., Pettersson U., Ergstrom A., Karlsson T., Bennich H.;
RT "Structure and evolution of the heavy chain from rat immunoglobulin
E.";
RL Nucleic Acids Res. 10:6041-6049 (1982).
RN [2]
RP SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162).
RX MEDLINE=83182019; PubMed=6820340;
RA Kindsvogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.;
RT "A cloned cDNA probe for rat immunoglobulin epsilon heavy chain:
construction, identification, and DNA sequence.";
RL DNA 1:335-343 (1982).
RN [3]
RP SEQUENCE OF 205-306 FROM N.A.
RX MEDLINE=82174576; PubMed=6803238;
RA Hellman L., Pettersson U., Bennich H.;
RT "Characterization and molecular cloning of the mRNA for the heavy
(epsilon) chain of rat immunoglobulin E.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268 (1982).
CC -!- SIMILARITY: Contains 4 immunoglobulin-like domains.
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CC
DR EMBL; J00744; AAA41379.1; ALT_INIT.
DR PIR; A93442; EHPT.
DR HSRF; P01854; LEP5.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig CL.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00407; IGL1; 1.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS0290; IG_MHC; 3.
KW Immunoglobulin C region; Immunoglobulin domain; Repeat.
FT NON_TER 1
FT DOMAIN 6 89 Ig-like 1.
FT DOMAIN 103 201 Ig-like 2.
FT DOMAIN 205 305 Ig-like 3.
FT DOMAIN 314 414 Ig-like 4.
FT CONFLICT 168 168 R -> N (in Ref. 2).
FT CONFLICT 308 308 P -> L (in Ref. 2).
SQ SEQUENCE 429 AA; 48671 MW; D2970B34EF8A72B0 CRC64;

Query Match 41.4%; Score 767.5; DB 1; Length 429;
Best Local Similarity 45.8%; Pred. No. 7.3e-51;
Matches 151; Conservative 54; Mismatches 114; Indels 11; Gaps 4;

QY 17 PVTIIPVTKLFHSCDPRGDAHSTIQLCLVSGFSPAKVHVTLVLDQAEANLFPYTR 76
Db 97 PVNITKPTVDLLHSSCDPNA-FHSTIQLYCPVYGHQNDVSIHMLMDRDI-----YETH 150
QY 77 PK---REGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSRKCADSNRGVSA 132
Db 151 AQNVLIKEGKLASTYSLRLNITQQWNSSTFTCKVTSQENYVAHTRSDDEPRGUIT 210
QY 133 YLSRSPFDLFIKRSPTITCLVVDLAPSKGTNLTWSRAGKPVNHSRKEEKQKNGILT 192
Db 211 YLIPSPDLVYENGTPKLTCLVLDL-ESEENITVTVRERKKSIGSASQSRSTKHNATTS 269
QY 193 VTSLPVGTRDWIEGETYQCRVTHPHLPALMRSTTKLPGLKLAPEVYVMLPPSEETGTT 252
Db 270 ITSILPVDKDWIEGEGYQCRVDPHPKPIVRSITKAPGRSAPEVYVFLPPPEEKDK 329
QY 253 RTVTCIRGFYPSISVQWLFNNEEDHTGHHTTTRPKQDGTDPSPFLYSRMLVYKSIWE 312
Db 330 RTLACLQNFPEDISVQWLQDSKLIKPSQHSITITPLKNGSNORFFISRLVTKALWT 389
QY 313 KGNLVTRCVVHEALPGSRTEKSLHYSA 342
Db 390 QTKQFTCKVHEALREPRKLERITKSLGN 419

RESULT 4
EPC_MOUSE ID EPC_MOUSE STANDARD; PRT; 421 AA.
AC P06336; P01856;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig epsilon chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN 11 SEQUENCE FROM N.A.
RP MEDLINE=84236092; PubMed=6329728;
RA Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T.;
RT "The nucleotide sequence of the mouse immunoglobulin epsilon gene:
RL comparison with the human epsilon gene sequence.";
EMBO J. 1:1117-1123(1982).
RN 12 [2]
RP REVISIONS.
RA Honjo T.;
RL Submitted (APR-1986) to the EMBL/GenBank/DBJ databases.
RN 13 [3]
RP SEQUENCE OF 34-421 FROM N.A.
RX MEDLINE=93117774; PubMed=6818553;
RA Liu F.-T., Albrandt K., Sutcliffe J.G., Katz D.H.;
RT "Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain
RL cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:7852-7856(1982).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X01857; CAA25977.1; -.
DR PIR; A02144; EHMS.
DR HSP; P01854; IPPS.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KW Glycoprotein; Immunoglobulin C region; Immunoglobulin domain.
FT DOMAIN 1 1 CH1.
FT DOMAIN 1 90 CH2.
FT DOMAIN 1 197 CH3.
FT DOMAIN 198 304 CH4.
FT DOMAIN 305 421 CH4.
FT DISULFID 23 75 By similarity.
FT DISULFID 121 180 By similarity.
FT DISULFID 226 285 By similarity.
FT DISULFID 330 392 By similarity.
FT CARBOHYD 43 43 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 72 72 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 84 94 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 95 95 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 166 166 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 238 238 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 261 261 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 365 365 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 415 415 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 421 AA; 47320 MW; 5F09E1F30A06B47 CRC64;
Query Match 40.5%; Score 751; DB 1; Length 421;
Best Local Similarity 44.8%; Pred. NO. 1.3e-49;
Matches 155; Conservative 53; Mismatches 130; Indels 8; Gaps 4;
QY 2 FHHHHHTLSPS-----GPTIIIPYVKLFHSSCDPRGDAHSTIQLLCLVSGSPAKV 56
Db 73 FTCHVTHPSFNSRILVRPNVITPTLELHSSCDPNA-FHSTIQLYCFYGHILNDV 131
QY 57 HVTVLVDGGEAENLFYTPTRKREGGQTFSLQSEVNITQGMSSNTYTCYKRNKGSIFE 116
Db 132 SVSWLMDREITDTLAQTVLKEE-CKLASTCKLNITEQQWSESTFTCKVTSQGVLY 190
QY 117 DSRKCADSNPRGSVAYLSRPSFDLFIKSTPTICLVLDLAPSNGTVNLWTSRAGRPV 176

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Db 191 AHTERCDFHBPGRGVITLYLPPSLDLYQNGAPKLTCLVLDSEK-NVNVWQEKTSV 249
QY 177 NHSTRKEEKORNGTLVTSITLPGVTRDWIEGTYQCRVTHPHLPRALMRSTTKLPKRLA 236
Db 250 SASQWYTKHNNATTSITSLPVVAKDWIEGYQCIVDHPDFPKIVRSITKTPQRS 309
QY 237 PEVYMLPSPPEETGTTRITVTCILIRGFYPSISVQWLFNNEEDTGHHTTTRPQKDGTD 296
Db 310 PEVYVFPPEESEDKTLTCLIQNFPEPDISVQWLDGDKLINSQSHSTTTPKLSNGSNQ 369
QY 297 SFFLYRMLYKSIWEKGNLVTCRVVHEALPGSRITLKSLSHYSAGN 342
Db 370 GFFIFSRLEVAKTLWTKQFTQVIEHALQKPKLEKTIISTSLGN 415

RESULT 5
MUCM_RABIT STANDARD; PRT; 479 AA.
AC P04221;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig mu chain C region membrane-bound form.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A. (A2 ALLOTYPE).
RX MEDLINE=8408930; PubMed=6418803;
RA Bernstein K.B., Alexander C.B., Reddy E.P., Mage R.G.;
RT "Complete sequence of a cloned cDNA encoding rabbit secreted mu-chain
RL of Vh2 allotype: comparisons with Vh1 and membrane mu sequences.";
J. Immunol. 132:490-495(1984).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=During differentiation, B lymphocytes switch from
CC expression of isoform Membrane-bound to isoform Secreted;
CC Name=Membrane-bound;
CC IsoId=P04221-1; Sequence=Displayed;
CC Name=Secreted;
CC IsoId=P03988-1; Sequence=External;
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
EMBL; X01357; AAA31293.1; -.
PIR; A02165; MHRBM.
HSSP; P01861; IADQ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_YHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KW Alternative splicing; Glycoprotein; Immunoglobulin C region;
KW Immunoglobulin domain; Transmembrane.
FT NON_TER 1 1
FT DOMAIN 1 106 CH1.
FT DOMAIN 107 222 CH2.
FT DOMAIN 223 327 CH3.
FT DOMAIN 328 458 CH4.
FT TRANSMEM 459 476 Potential.
FT DISULFID 14 14 Interchain (with light chain) (Probable).
FT DISULFID 28 90 By similarity.
FT DISULFID 137 200 By similarity.

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FT DISULFID 219 Interchain (with heavy chain) (Probable).
FT DISULFID 249 By similarity.
FT DISULFID 296 Interchain (with heavy chain) (Probable).
FT DISULFID 356 418 By similarity.
FT CARBOHYD 46 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 114 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 212 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 261 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 277 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 284 N-linked (GLCNAC...) (Potential).
SQ SEQUENCE 479 AA; 52351 MW; 689C637A47BE19FC CRC64;

Query Match
Best Local Similarity 26.8%; Score 497.5; DB 1; Length 479;
Matches 117; Conservative 61; Mismatches 153; Indels 25; Gaps 10;

QY 5 HHHTLSLPSGVP-TIIPTVKLPFHSSCDPR----GDAHSTTQLLCLVSGSPAKVHYT 59
DB 94 HNSNRDLRVSPFDSELPNVSVF---IPRDSFGSGTRKSRLLICQATGSPKQISVS 150

QY 60 WLVDDQGEAEN---LFPYTPPKREGGOTSLQSEVNITQGMSSNTYTCVKNHNGSIFE 116
DB 151 WLDDGQKVESGLVTKPVAETKAGPATFSISSMLTITSDLSQSLYTCRDVHRGIFD 210

QY 117 DS---SRKCADSNPRGVSAYLSRPSPDLPFRKSPITTCVLVDLAPSKGTNLTWRASG 173
DB 211 KNVMSSECTTSPGLOVPIAPSPADTFLSKASRLICLVTDLT-TYGLNISWASHNG 269

QY 174 KPNVHSTRKEEKORNGTLTVSTLTPVGTDRWIEGTQYQCRVTHPHLPALMRSTTKLPQK 233
DB 270 KALDTHMNITESHNPATFSAMGEASVCAEDWESGEQFTCTVTHADLPFLKHTISK--SR 327

QY 234 RLA---PEVYMLPPSPPE--TGTRTVTCILRGVPSSEISVQWLFNNEEDTGHHTTTP 288
DB 328 EVAKHPAVVLPAREQLVRESAIVTCLVKGSPADVPVQMQQGQLSSDKYVTSAP 387

QY 289 QKDHTGDPSPFLYSLMLVKNKSIWEKGNLVTCTRVVHEALP---GSRLEKSLHYSAG 341
DB 388 APEQPAGLYTHSTLTVTEEDWNSGETFTCVVGHEALPHMVTERTVDKSTGEVG 443

RESULT 6
Q6MZU6 PRELIMINARY; PRT; 464 AA.
AC Q6MZU6;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C15213.
GN Name=DKFZp686C15213;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640874; CAE45931.1; -.
KW Hypothetical protein.
SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C66E8A0ABC CRC64;

Query Match
Best Local Similarity 26.8%; Score 496.5; DB 2; Length 464;
Matches 118; Conservative 58; Mismatches 118; Indels 29; Gaps 11;

QY 35 RGAHSTTQLLCLVSGSPAKVHYTW---LVDQGEAENLFPYTPRKREGGOTFSLQSE 90
DB 154 RSTSESTVALGCLVKDYPPEPTVSWNSGALTSG---VHTPPAVL-----QSSGLYSLSSV 206

QY 91 VNITQGMSSNTYTCVKNH---NGSIFEDSSRRCADSNP-----RGVSAYLSRSPFP 140
DB 207 VVTSSNF-GTQYTCNVVDHKPSNTKVDKTVKRCCKVECPCCPAPPVAGSVPLFPPKPK 265

QY 141 D-LFIRKSPITTCVLVDLAPSKGTNLTWRASGKPVNHSRKEEKORNGTLTVSTLTPV 199
DB 266 DTLMSRTPETVTCVVDVSHEDPEVQFNWYVDGMEVHNNAKTKPREEQFNSTFRVSVLTV 325

QY 200 GTRDWIEGTQYQCRVTHPHLPALMRSTTKLPGRLAPEVYMLPPSPPE--TGTRTVTC 258
DB 326 VHQDWLNGKEYCKCKVKNKGLPAPIEKTIKTGQPREPQVYTLPPSREEMTKNQVSLTCL 385

QY 259 IRGFYPSISVQWLFNNEEDTGHHTTTPRQKDHGTDPSPFLYSLMLVKNKSIWEKGNLVT 318
DB 386 VKGFYPSDIWVESNGQPEN--NYKTPPMLD--SDGSFELYSLKLTVDKSRWQGNVFS 441

QY 319 CRVHEALPGSRITLEKSLHYSAG 341
DB 442 CSMHEALHNYT-QKSLSLSPG 463

RESULT 7
CAE45931 PRELIMINARY; PRT; 464 AA.
AC CAE45931;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C15213.
GN DKFZp686C15213.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640874; CAE45931.1; -.
KW Hypothetical protein.
SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C66E8A0ABC CRC64;

Query Match
Best Local Similarity 36.5%; Pred. No. 6.2e-30;
Matches 118; Conservative 58; Mismatches 118; Indels 29; Gaps 11;

QY 35 RGAHSTTQLLCLVSGSPAKVHYTW---LVDQGEAENLFPYTPRKREGGOTFSLQSE 90
DB 154 RSTSESTVALGCLVKDYPPEPTVSWNSGALTSG---VHTPPAVL-----QSSGLYSLSSV 206

QY 91 VNITQGMSSNTYTCVKNH---NGSIFEDSSRRCADSNP-----RGVSAYLSRSPFP 140
DB 207 VVTSSNF-GTQYTCNVVDHKPSNTKVDKTVKRCCKVECPCCPAPPVAGSVPLFPPKPK 265

QY 141 D-LFIRKSPITTCVLVDLAPSKGTNLTWRASGKPVNHSRKEEKORNGTLTVSTLTPV 199
DB 266 DTLMSRTPETVTCVVDVSHEDPEVQFNWYVDGMEVHNNAKTKPREEQFNSTFRVSVLTV 325

QY 200 GTRDWIEGTQYQCRVTHPHLPALMRSTTKLPGRLAPEVYMLPPSPPE--TGTRTVTC 258
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Db 177 VSNNGALTSQ---VHTFPAVL-----QSSGLYSLSSVTVTPSSNF-GTQTYTNCVHKPS 228
QY 111 NGSTFEDSRKADSNP-----RGVSAYLSRSPSPD-LFIRKSPITICLVVDLAPSKG 162
Db 229 NTKVDKTVRKCCEPCPCAPPVAGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDP 288
QY 163 TVNLWTSRASKPVNHSRKEKQNGTLTVSTPLVGTDRWTEGETYQCRVTHPLPRA 222
Db 289 EVQFNWYDVEVHNATKREDFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAP 348
QY 223 LMRSTTKLPGRKLAPVYMLPPSPPEE-TGTRTVTCILIRGFYSPSEISVQWLFNNEEDHTG 281
Db 349 IEKTSIKTKGPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN-- 406
QY 282 HHTTRPQKHGTDPSFELYSRMLVKNKSIWEKGNLVTCTRVHVALPGSRITLKSLSHSAG 341
Db 407 NYKTTPEMLD--SDGSFFLYSKLTVDSRWQOQNVFSCVYHAEALHNHYT-QKSLSLSPG 463

RESULT 10
ID BAC85483 PRELIMINARY; PRT; 468 AA.
AC BAC85483;
DT 02-MAR-2004 (TReMBLrel. 27, Created)
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
DE CDNA FLJ29011 fis, clone DMC03382, highly similar to Ig gamma-2 chain
DE C region (Human)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Dermoid tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RX "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
RL [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062335; AAH62335.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 468 AA; 51715 MW; CB3A94413B6C36CA CRC64;

Query Match 26.6%; Score 493.5; DB 2; Length 468;
Best Local Similarity 34.7%; Pred. No. 1.1e-29;
Matches 124; Conservative 66; Mismatches 134; Indels 33; Gaps 13;

QY 5 HHHTLSLPESG-PVTIIPPTVK---LFHSSCDPRGDAHSTIQLLCLVSGFSAPKVVHTW 60
Db 124 IYIIGLDVWGQGPVTVSTASTKGPSVFLPAPCSRSTSESTAALGCLVXDYFPEPVTVM 183
QY 61 ----LVDAQEALFPYTTTRPKREGGTFSLQSEVNTIQQWMSNTYTCVHKH---NGS 113
Db 184 NSGALTSQ---VHTFPAVL-----QSSGLYSLSSVTVTPSSNF-GTQTYTNCVHKPSNTK 235
QY 114 IFDSSRKADSNP-----RGVSAYLSRSPSPD-LFIRKSPITICLVVDLAPSKGTVN 165
Db 236 VDKTVRKCCEPCPCAPPVAGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVQ 295
QY 166 LTWSRASKPVNHSRKEKQNGTLTVSTPLVGTDRWTEGETYQCRVTHPLPALMR 225
Db 296 FNNYVDGVEVHNATKREDFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEK 355
QY 226 STTKLPKRLAPVYMLPPSPPEE-TGTRTVTCILIRGFYSPSEISVQWLFNNEEDHTGHT 284
Db 356 TISKTKGPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN--NYK 413
QY 285 TTRPQKHGTDPSFELYSRMLVKNKSIWEKGNLVTCTRVHVALPGSRITLKSLSHSAG 341
Db 414 TTPPEMLD--SDGSFFLYSKLTVDSRWQOQNVFSCVYHAEALHNHYT-QKSLSLSPG 467
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RESULT 11
Q6P6C4
ID Q6P6C4 PRELIMINARY; PRT; 465 AA.
AC Q6P6C4;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RX "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
RL [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062335; AAH62335.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51325 MW; FDDB9348ADC37E6D CRC64;

Query Match 26.3%; Score 488.5; DB 2; Length 465;
Best Local Similarity 35.0%; Pred. No. 2.6e-29;
Matches 124; Conservative 61; Mismatches 130; Indels 39; Gaps 13;

QY 7 HHTLSLPESGVTIIPPTVK---LFHSSCDPRGDAHSTIQLLCLVSGFSAPKVVHTW--- 60
Db 131 HGTL-----VTSSASTKGPSVFLPAPCSRSTSESTAALGCLVXKQYFPEPVTVMNSG 183
QY 61 -LVDAQEALFPYTTTRPKREGGTFSLQSEVNTIQQWMSNTYTCVHKH---NGSIFE 116
Db 184 ALTSQ---VHTFPAVL-----QSSGLYSLSSVTVTPSSNF-GTQTYTNCVHKPSNTKVDK 235
QY 117 DSSRKADSNP-----RGVSAYLSRSPSPD-LFIRKSPITICLVVDLAPSKGTVNLTW 168
Db 236 TVRKCCEPCPCAPPVAGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNW 295
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236 TVRKKCCVPCPAPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNW 235
169 SRASGKPVNHSRKEEKQKNGTLTVSTLPVGTDRWIEGETYOCRVTHPHLPALMRSTT 228
296 YVDGVEVHNAKTPREEQNSTFRVSVLTVVHQDWLNGKEYCKVSNKGLPAPIEKTIS 355
229 KLPGRKLAPEVYMLPPSPPEE-TGTTTRTVTCLIRGFYPSISVQWLFNNEEDHTGHHTTR 287
356 KTKGQPREPOVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVWESNGOPEN--NNTTTP 413
288 PQKHGTDPSFFLYSRMLVKNKSWKGNLTVCRVHEALPGSRTLEKSLHYSAG 341
414 PMLD--SDGSFFLYSKLTVDKSRWQQGVFSCVMHEALHNYT-QKSLSLSPG 464

Db QY Db QY Db QY
QY Db QY
QY Db QY
Db QY
Db QY

RESULT 13
GC2_HUMAN
ID GC2_HUMAN STANDARD; PRT; 326 AA.
AC P01859;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig gamma-2 chain C region.
GN Name=IGHG2;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 2-326 FROM N.A.
RX MEDLINE=82197621; PubMed=6804948;
RA Ellison J.W., Hood L.E.;
RT "Linkage and sequence homology of two human immunoglobulin gamma heavy
chain constant region genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988 (1982).
RN [2]
RP SEQUENCE OF 88-115 FROM N.A.
RX MEDLINE=83001943; PubMed=6811139;
RA Takahashi N., Ueda S., Obata M., Nikaide T., Nakai S., Honjo T.;
RT "Structure of human immunoglobulin gamma genes: implications for
evolution of a gene family.";
RL Cell 29:671-679 (1982).
RN [3]
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RX TISSUE=Fetal liver;
RX MEDLINE=84235992; PubMed=6329676;
RA Krawinkel U., Rabbitts T.H.;
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
genes";
RL EMBO J. 1:403-407 (1982).
RN [4]
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX MEDLINE=81007873; PubMed=6774012;
RA Wang A.-C., Tung E., Fudenberg H.H.;
RT "The primary structure of a human IgG2 heavy chain: genetic,
evolutionary, and functional implications.";
RL J. Immunol. 125:1048-1054 (1980).
RN [5]
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX MEDLINE=80001357; PubMed=113060;
RA Connell G.E., Parr D.M., Hofmann T.;
RT "The amino acid sequences of the three heavy chain constant region
domains of a human IgG2 myeloma protein.";
RL Can. J. Biochem. 57:758-767 (1979).
RN [6]
RP SEQUENCE OF 238-275 (ZIE).
RX MEDLINE=80114419; PubMed=118920;
RA Hofmann T., Parr D.M.;
RT "A note of the amino acid sequence of residues 381-391 of human
immunoglobulin gamma chains.";
RL Mol. Immunol. 16:923-925 (1979).

AAH62335 PRELIMINARY; PRT; 465 AA.
AC AAH62335;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Spleen;
RX MEDLINE=23388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E.,
Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszinski M.I., Skalek U., Smallos D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062335; AAH62335.1;
RW Hypothetical protein.
SQ SEQUENCE 465 AA; 51325 MW; FDDB9348ADC3736D CRC64;

Query Match 26.3%; Score 488.5; DB 2; Length 465;
Best Local Similarity 35.0%; Pred. No. 2.6e-29;
Matches 124; Conservative 61; Mismatches 130; Indels 39; Gaps 13;
QY 7 HTTSLPESGPVITIPPTVK---LFHSSCDPRGDAHTIOLLCLVSGFSPAKVHTVW--- 60
Db 131 HGTL-----VTSSASTKGPSVFLPACRSRSTSESTAALGCLVKDYFPFVTVSNWNG 183
QY 61 -LVDPQEAENLFPYTRPRKGGTFTSLQSEVNITQGMSSNTYCHVKH---NGSIFE 116
Db 184 ALTSG---VHTFPAVL---QSSGLYSLSSVTVTPSPNF-GTQTYTCNVDDHKPSNPKVDK 235
QY 117 DSSPKCADSNP-----RGVSAYLSRPSFPD-LFRKSTTICLVVDLAPSGKGTNLTW 168

[7]
RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
RA Hofmann T., Parr D.M.;
RL Submitted (VAR-1980) to the PIR data bank.
[8]
RP SEQUENCE OF 1-121 (DOT).
RP MEDLINE=95255298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin mononuclear
immunoglobulins.";
RL Eur. J. Biochem. 228:886-893 (1995).
[9]
RP DISULFIDE BONDS.
RP MEDLINE=72033500; PubMed=4940472;
RA Milstein C., Frangione B.;
RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
RL Biochem. J. 121:217-225 (1971).
[10]
RP DISULFIDE BONDS.
RP MEDLINE=69064124; PubMed=5782707;
RA Frangione B., Milstein C., Pink J.R.L.;
RT "Structural studies of immunoglobulin G.";
RL Nature 221:145-148 (1969).
[11]
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[12]
CC EMBL; J00230; AAB59393.1; -.
DR PIR; A93906; G2HU.
DR HSP; P01857; 100X.
DR Genew; HGNC:5526; IG2G2.
DR MM; 147110; -.
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IG1; 2.
DR PROSITE; PS00290; IG_MHC; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain
FT NON TER 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 Hinge.
FT DOMAIN 111 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 14 14 Interchain (with a light chain).
FT DISULFID 27 83 Interchain (with a heavy chain).
FT DISULFID 102 102 Interchain (with a heavy chain).
FT DISULFID 103 103 Interchain (with a heavy chain).
FT DISULFID 106 106 Interchain (with a heavy chain).
FT DISULFID 109 109 Interchain (with a heavy chain).
FT DISULFID 140 200
FT DISULFID 246 304
FT DISULFID 156 156
FT SITE
FT VARIANT 60 60
FT CONFLICT 109 109
FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;
AT OR NEAR THE COMPLEMENT-BINDING SITE.
S -> A (in myeloma proteins TIL and ZIE).
C -> S (in Ref. 3).
/FTID:VAR_003889.
Query Match 26.2%; Score 486.5; DB 1; Length 326;
Best Local Similarity 36.2%; Pred. No. 2.4e-29;
Matches 117; Conservative 57; Mismatches 120; Indels 29; Gaps 11;
35 RGDASTIQLLCLVSGFSPAKVHTW----LVDQAEALNFPYTRPRKGGQTFSLQSE 90

Db 16 RSTSESTAALGCLVKDYFPEPTVWSNLSGALTSG---VHTFPAVL-----QSSGLYSLSV 68
Qy 91 VNITQGQWMSNTYTCHVKH---NGSIPEDSSRKCADSNP-----RGVSAYLSRPSPP 140
Db 69 VTPSSNF-GTQTYTCNVHDHPSNTKVDKTVKRCVCEPCPCAPPVAGPSVFLPPKPK 127
Qy 141 D-LFTRKSPPTTCLVVDLAPSKGTVNLWTSRASGKPVNHSRKEKQKRGNTLTVTSTLPV 199
Db 128 DTLMT-SRTPEVTVCVVVDVSHEDPEVQFNWYVDGVEVHNNAKTKPREEQFNSTFRVVSULTV 187
Qy 200 GTRDWIEGTYQCRVTHPLRALMRSTTKLPGLAPEVYMLPSPPEE-TGTRIVTCL 258
Db 198 VHQDWLNGKEYKCKVSNKGLPAPIEKTSKTKGPREPQVYTLPPSREMTKNQVSLTCL 247
Qy 229 IRGTFPSSISVQWLFNNEEDHTGHHTTRPKDHTGTPSPFLYSLMLVKNKINWKGNTLV 318
Db 248 VKGFYPSDIAVEWESNGQFEN--NYKTTTPMLD--SDGSFFLYSKLTVDKSRWQGNVFS 303
Qy 319 CRVVHEALPGSRTLEKSLHYSAG 341
Db 304 CSVMHEALHNHYT-QKSLSLSPG 325
RESULT 14
Q6N093 PRELIMINARY; PRT; 417 AA.
AC Q6N093;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686i04196 (Fragment).
GN Name=DKFZp686i04196;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG THE GERMAN HUMAN CDNA CONSORTIUM;
RA Wambutt R., Haubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640623; CAE45777.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON TER 1
FT SEQUENCE 417 AA; 46061 MW; C4518E844CFB883C CRC64;
Query Match 26.2%; Score 486.5; DB 2; Length 417;
Best Local Similarity 36.2%; Pred. No. 3.2e-29;
Matches 117; Conservative 57; Mismatches 120; Indels 29; Gaps 11;
Qy 35 RGDASTIQLLCLVSGFSPAKVHTW----LVDQAEALNFPYTRPRKGGQTFSLQSE 90
Db 107 RSTSESTAALGCLVKDYFPEPTVWSNLSGALTSG---VHTFPAVL-----QSSGLYSLSV 159
Qy 91 VNITQGQWMSNTYTCHVKH---NGSIPEDSSRKCADSNP-----RGVSAYLSRPSPP 140
Db 160 VTPSSNF-GTQTYTCNVHDHPSNTKVDKTVKRCVCEPCPCAPPVAGPSVFLPPKPK 218

QY 141 D-LPIKSPITICLVVDLAPSKGTNLTWSRASKGKPVNHSRKEEKORNGTLTSTLTPV 199
Db 219 DTLMSIRTPETVCVVDVSHEDDEVQFNWYDGVVHNKTKPREQFNSTFRVVSVLTV 278
QY 200 GTRDWIEGETYQCRVTHPLPRALMRSTTKLPGKRLAPEVYMLPPSPPEE-TGTRTVTCL 258
Db 279 VHQDWLNGKEYKCKVSKNGKLPAPIEKTIKTGQPREQPVYTLPPSREEMTKNQVSLTCL 338
QY 259 IRGFYPSSEISVQMLFNNEEDHTGHTTTPQKDHGTDPSFFLYSRMLVNKSIWEKGNLVT 318
Db 339 VKGFYPSDIAVENESNGQPN--NYKTPPMLD--SDGSFFLYSKLTVDKSRWQGNVFS 394
QY 319 CRVVHEALPGSRILEKSLHYSAG 341
Db 395 CSVMHEALHNHYT-QKSLSLSPG 416

RESULT 15

CAE45777
ID CAE45777 PRELIMINARY; PRT: 417 AA.
AC CAE45777;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DI 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DI 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686I04196 (Fragment).
GN DKFZP686I04196.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [2]
RP SEQUENCE FROM N.A.
RC T-SSUE=Human esophagus tumor;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640823; CAE45777.1; -
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 417 AA; 46061 MW; C4518E844CFB893C CRC64;

Query Match 26.2%; Score 486.5; DB 2; Length 417;
Best Local Similarity 36.2%; Pred. No. 3.2e-29;
Matches 117; Conservative 57; Mismatches 120; Indels 29; Gaps 11;

QY 35 RGDHSTIQLLCLVSGFSPAKVHTW----LVDGQAEMLFPYTRPKREGGOTPSLQSE 90
Db 107 RSTSESTAALGCLVXDYFPEPVTVMNSGALTSG--VHTFPAVL----QSSGLYSLSSV 159
QY 91 VNITQGMMSNTYTCVHKH--NGSIFEDSSRKCADSNP-----RGVSAYLSRSPSF 140
Db 160 VTVPSSNF-GTQYTCNVNDHKPNKTVKVERKCCVECPCPAPVAGPSVFLFPKPK 218
QY 141 D-LPIKSPITICLVVDLAPSKGTNLTWSRASKGKPVNHSRKEEKORNGTLTSTLTPV 199
Db 219 DTLMSIRTPETVCVVDVSHEDDEVQFNWYDGVVHNKTKPREQFNSTFRVVSVLTV 278
QY 200 GTRDWIEGETYQCRVTHPLPRALMRSTTKLPGKRLAPEVYMLPPSPPEE-TGTRTVTCL 258
Db 279 VHQDWLNGKEYKCKVSKNGKLPAPIEKTIKTGQPREQPVYTLPPSREEMTKNQVSLTCL 338
QY 259 IRGFYPSSEISVQMLFNNEEDHTGHTTTPQKDHGTDPSFFLYSRMLVNKSIWEKGNLVT 318
Db 339 VKGFYPSDIAVENESNGQPN--NYKTPPMLD--SDGSFFLYSKLTVDKSRWQGNVFS 394
QY 319 CRVVHEALPGSRILEKSLHYSAG 341
Db 395 CSVMHEALHNHYT-QKSLSLSPG 416

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: November 14, 2004, 14:55:18 ; Search time 157 Seconds
(without alignments)
781.436 Million cell updates/sec

Title: US-09-401-636-8
Perfect score: 1856
Sequence: 1 EFHHHTLSLPESQPTV.....HEALPGSRTLEKSLHYSAGN 342

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq_23Sep04:.*
1: Geneseqp1980s:.*
2: Geneseqp1980s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1856	100.0	342	3 AAB06205	Aab06205 Immunogen
2	1786	96.2	338	8 ADF90025	Adf90025 Opossum-h
3	1786	96.2	338	8 ADN00646	Adn00646 OSO prote
4	1786	96.2	347	8 ADF90033	Adf90033 Opossum-h
5	1786	96.2	347	8 ADN00654	Adn00654 OSO-H pro
6	1772	95.5	557	8 ADF90031	Adf90031 Opossum-h
7	1772	95.5	557	8 ADF90035	Adf90035 Opossum-h
8	1772	95.5	557	8 ADN00656	Adn00656 OSO pro
9	1772	95.5	557	8 ADN00652	Adn00652 modOSO
10	1772	95.5	566	8 ADF90029	Adf90029 Opossum-h
11	1772	95.5	566	8 ADF90037	Adf90037 Opossum-h
12	1772	95.5	566	8 ADN00658	Adn00658 OSO-H p
13	1772	95.5	566	8 ADN00650	Adn00650 modOSO
14	1759	94.8	353	8 ADN00661	Adn00661 H-OCO-H p
15	1644.5	88.6	341	3 AAB06208	Aab06208 Immunogen
16	1587.5	85.5	345	3 AAB06207	Aab06207 Immunogen
17	1584.5	85.4	341	3 AAB03644	Aab03644 Opossum I
18	1583.5	84.5	341	3 AAB06206	Aab06206 Immunogen
19	1523.5	82.1	446	6 ABP96587	Abp96587 Opossum I
20	1498.5	80.7	337	8 ADF90022	Adf90022 Opossum-h
21	1498.5	80.7	337	8 ADN00643	Adn00643 ORO prote
22	1486.5	80.1	555	8 ADF90027	Adf90027 Opossum-r
23	1486.5	80.1	555	8 ADN00648	Adn00648 ORORO pro
24	1392.5	75.0	341	3 AAB06202	Aab06202 Immunogen
25	1375	74.1	342	3 AAB06201	Aab06201 Immunogen

26	1285.5	69.3	427	6 ABP96591	Abp96591 Brugstail
27	1045.5	56.3	569	6 AAO19668	Aao19668 GE2 fusio
28	1044	56.2	577	6 ABP96584	Abp96584 Duckbille
29	1038.5	56.0	320	6 AAO19667	Aao19667 Human IGE
30	1038.5	56.0	323	5 AAU80286	Aau80286 Human IGE
31	1038.5	56.0	323	5 AAU80285	Aau80285 Human IGE
32	1038.5	56.0	323	5 AAU80284	Aau80284 Human IGE
33	1038.5	56.0	324	2 AAR83559	Aar83559 Fc(epsilo
34	1038.5	56.0	325	2 AAR75225	Aar75225 Human IGE
35	1038.5	56.0	325	2 AAR77241	Aar77241 Human IGE
36	1038.5	56.0	331	3 AAB03642	Aab03642 Human IGE
37	1038.5	56.0	331	7 ADD25768	Add25768 Binding d
38	1038.5	56.0	367	1 AAP80291	Aap80291 Interleuk
39	1038.5	56.0	427	6 AAO19666	Aao19666 Human IGE
40	1038.5	56.0	428	5 AAM47863	Aam47863 Human IGE
41	1038.5	56.0	428	5 AAU80283	Aau80283 Human IGE
42	1038.5	56.0	428	5 AAM50940	Aam50940 Human IGE
43	1038.5	56.0	428	6 AAE35113	Aae35113 Human Imm
44	1038.5	56.0	428	7 ADD48440	Add48440 Human pro
45	1038.5	56.0	428	7 ADE97382	Ade97382 Human IGE

ALIGNMENTS

RESULT 1

AAB06205
ID AAB06205 standard; protein; 342 AA.

AC AAB06205;

XX

DT 12-SEP-2003 (revised)

DT 22-NOV-2000 (first entry)

XX

DE Immunogenic peptide consisting of opossum CH2, human CH3 and opossum CH4.

XX

KW Human; opossum; immunoglobulin E; IGE; vaccination; infection; allergy;

KW asthma; eczema; immunogenic peptide.

XX

OS Didelphis virginiana.

OS Homo sapiens.

OS Chimeric.

XX

PN WO200025722-A2.

XX

PD 11-MAY-2000.

XX

PF 21-OCT-1999; 99WO-SE001896.

XX

PR 02-NOV-1998; 98US-0106652P.

PR 22-SEP-1999; 99US-00401636.

XX

PA (RESI-) RESISTENTIA PHARM AB.

XX

PI Hellman LT;

XX

WPI; 2000-365342/31.

XX

Immunogenic polypeptides useful for preventing the harmful effects of immunoglobulin E in mammals.

XX

Disclosure; Fig 2; 50pp; English.

XX The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2 and 4 of the opossum IGE and the heavy chain constant region 3 from the human. It was shown to cause a stronger polyclonal anti-self IGE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema. (Updated on 12-SEP-2003 to standardise OS field)

XX

SQ Sequence 342 AA;
 Query Match 100.0%; Score 1856; DB 3; Length 342;
 Best Local Similarity 100.0%; Pred. No. 5.4e-146;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFHHHHHTLSLPSGPTTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW 60
 DB 1 EFHHHHHTLSLPSGPTTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW 60
 QY 61 LVDCQEAENIFPVTTRPKREGGQTFSLQSEVNTIQQWSSNTYTCHVKHNGSIFEDSSR 120
 DB 61 LVDCQEAENIFPVTTRPKREGGQTFSLQSEVNTIQQWSSNTYTCHVKHNGSIFEDSSR 120
 QY 121 KCADSNPRGVSAYLSRSPFDLFIKSPPTIICLVDLAPSKGTNLTWSRASKPVNHST 180
 DB 121 KCADSNPRGVSAYLSRSPFDLFIKSPPTIICLVDLAPSKGTNLTWSRASKPVNHST 180
 QY 181 RKEKQKNGTLVTSTLPVGTDRWIEGETYQCRVTHPLPALMRSTTKLPGRLAPEVY 240
 DB 181 RKEKQKNGTLVTSTLPVGTDRWIEGETYQCRVTHPLPALMRSTTKLPGRLAPEVY 240
 QY 241 MLPSPPEETGTRITVTCILIRGFYPSISVQWLFNNEEDHTGHTTTRPQKDHGTDPSPFL 300
 DB 241 MLPSPPEETGTRITVTCILIRGFYPSISVQWLFNNEEDHTGHTTTRPQKDHGTDPSPFL 300
 QY 301 YSRMLNKSWEKGNLVTQVWHEALPGSRTLEKSLHYSAGN 342
 DB 301 YSRMLNKSWEKGNLVTQVWHEALPGSRTLEKSLHYSAGN 342

RESULT 2
 ADF90025
 ID ADF90025 standard; protein; 338 AA.
 XX AC ADF90025;
 XX DT 26-FEB-2004 (first entry)
 XX DE Opossum-human chimeric IgE polypeptide.
 XX KW IgE; immunoglobulin; antibody; opossum; human; vaccine; antiallergic;
 XX KW antiasthmatic; dermatological.
 XX OS Chimeric.
 XX OS Didelphis virginiana.
 XX OS Homo sapiens.
 XX PN WO2003096966-A2.
 XX PD 27-NOV-2003.
 XX PF 15-MAY-2003; 2003WO-IB002503.
 XX PR 21-MAY-2002; 2002US-0382552P.
 XX PA (RESI-) RESISTENTIA PHARM AB.
 XX PI Lundgren M, Fuentes A, Magnusson A;
 XX DR WPI; 2004-042496/04.
 XX DR N-PSDB; ADF90024, ADF90023.
 XX PT New host cell comprising a nucleic acid vector comprising a
 PT cytomagalovirus promoter, an Ig leader sequence, an insert sequence or
 PT SV40 late polyadenylation sequence, useful in producing a chimeric IgE
 PT polypeptide.
 XX PS Claim 3; SEQ ID NO 6; 23pp; English.
 XX CC The present sequence is the protein sequence of an opossum CH2-human CH3-
 CC opossum CH4 (OSO) chimeric IgE polypeptide. A vector comprising DNA
 CC encoding OSO can be used for recombinant production this chimeric IgE in

CC host, e.g. CHO, cells. The invention provides methods and materials
 CC related to expressing chimeric IgE proteins. Nucleic acid vectors, host
 CC cells, and methods for producing chimeric IgE polypeptides are provided.
 CC When administered to a mammal, the chimeric polypeptides can reduce the
 CC IgE antibody effects of IgE-related diseases such as asthma, allergies
 CC and eczema.
 XX SQ Sequence 338 AA;
 Query Match 96.2%; Score 1786; DB 8; Length 338;
 Best Local Similarity 99.4%; Pred. No. 3.6e-140;
 Matches 334; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 9 TSLSPESGPTTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTWLDGQEA 68
 DB 3 TSLSPESGPTTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTWLDGQEA 62
 QY 69 NLFYTTTRPKREGGQTFSLQSEVNTIQQWSSNTYTCHVKHNGSIFEDSSRKCADSNPR 128
 DB 63 NLFYTTTRPKREGGQTFSLQSEVNTIQQWSSNTYTCHVKHNGSIFEDSSRKCADSNPR 122
 QY 129 GVSAYLSRSPFDLFIKSPPTIICLVDLAPSKGTNLTWSRASKPVNHSTKEKQKRN 198
 DB 123 GVSAYLSRSPFDLFIKSPPTIICLVDLAPSKGTNLTWSRASKPVNHSTKEKQKRN 182
 QY 189 GTLVTSTLPVGTDRWIEGETYQCRVTHPLPALMRSTTKLPGRLAPEVYMLPPSP 246
 DB 183 GTLVTSTLPVGTDRWIEGETYQCRVTHPLPALMRSTTKLPGRLAPEVYMLPPSP 242
 QY 247 BETGTTRVTCILIRGFYPSISVQWLFNNEEDHTGHTTTRPQKDHGTDPSPFLYSRMLV 306
 DB 243 BETGTTRVTCILIRGFYPSISVQWLFNNEEDHTGHTTTRPQKDHGTDPSPFLYSRMLV 302

QY 307 NKSWEKGNLVTQVWHEALPGSRTLEKSLHYSAGN 342
 DB 303 NKSWEKGNLVTQVWHEALPGSRTLEKSLHYSAGN 338

RESULT 3
 ADF900646
 ID ADF900646 standard; protein; 338 AA.
 XX AC ADF900646;
 XX DT 17-JUN-2004 (first entry)
 XX DE OSO protein, SEQ ID 6.
 XX KW Antiallergic; Vaccine; self-IgE; OSO; allergy.
 XX OS Synthetic.
 XX PN WO2004022094-A1.
 XX PD 18-MAR-2004.
 XX PF 02-JUN-2003; 2003WO-IB003075.
 XX PR 05-SEP-2002; 2002US-0408648P.
 XX PA (RESI-) RESISTENTIA PHARM AB.
 XX PI Hellman LT, Persson S, Gansson A;
 XX DR WPI; 2004-248376/23.
 XX DR N-PSDB; ADF900645.
 XX PT New composition comprising a self-IgE polypeptide and an aluminum
 PT compound, useful for inducing an anti self-IgE antibody response in a
 PT mammal for treating or preventing allergies.
 XX PS Claim 3; Fig 8; 102pp; English.

CC The present invention relates to a composition comprising a polypeptide
 CC and an aluminum compound, where the polypeptide comprises a self-IgE
 CC polypeptide sequence (e.g., an ORO polypeptide or an OSO polypeptide;
 CC ADN00643, ADN00646, ADN00650, ADN00652, ADN00654, ADN00656, ADN00658 or
 CC ADN00661). Administration of the composition to a mammal reduces the
 CC level of detectable free IgE in the mammal. The composition is useful for
 CC inducing an anti self-IgE antibody response in a mammal for treating or
 CC preventing allergies. The present sequence is an OSO protein, used to
 CC illustrate the invention. The OSO protein contains an opossum CH2 IgE
 CC domain followed by a human CH3 IgE domain followed by an opossum CH4 IgE
 CC domain.

XX SQ Sequence 338 AA;
 CC Query Match 96.2%; Score 1786; DB 8; Length 338;
 CC Best Local Similarity 99.4%; Pred. No. 3.6e-140;
 CC Matches 334; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
 QY 9 TSLSPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTLVVDQGEAE 68
 DB 3 TSLSPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTLVVDQGEAE 62
 QY 69 NLPFYTRPKREGGQTFSLQSEVNI TOGWSSNTYTCHVKHNGSIFEDSSRKCADSNPR 128
 DB 63 NLPFYTRPKREGGQTFSLQSEVNI TOGWSSNTYTCHVKHNGSIFEDSSRKCADSNPR 122
 QY 129 GVSAYLSRSPFDFIRKSPITITCLVVDLAPSKGTVNLWTSRAGKPVNHSTRKEEKORN 188
 DB 123 GVSAYLSRSPFDFIRKSPITITCLVVDLAPSKGTVNLWTSRAGKPVNHSTRKEEKORN 182
 QY 189 GTLVTSTLPVGTREDWIEGTQYCRVTHPLPALMRSTTKL--PGKRLAPEVYMLPPSP 246
 DB 183 GTLVTSTLPVGTREDWIEGTQYCRVTHPLPALMRSTTKL--PGKRLAPEVYMLPPSP 242
 QY 247 EETGTRTRVTCILIRGFYPSISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFLYSRMLV 306
 DB 243 EETGTRTRVTCILIRGFYPSISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFLYSRMLV 302
 QY 307 NKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342
 DB 303 NKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 338

RESULT 4
 ADF90033
 ID ADF90033 standard; protein; 347 AA.
 AC ADF90033;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Opossum-human chimeric IgE polypeptide.
 XX
 KW IgE; immunoglobulin; antibody; opossum; human; vaccine; antiallergic;
 KW antiasthmatic; dermatological.
 XX
 OS Chimeric.
 OS Didelphis virginiana.
 OS Homo sapiens.
 XX
 PN W02003096966-A2.
 XX
 PD 27-NOV-2003.
 XX
 PF 15-MAY-2003; 2003WO-IB002503.
 XX
 PR 21-MAY-2002; 2002US-0382552P.
 XX
 PA (RESI-) RESISTENTIA PHARM AB.
 XX
 PI Lundgren M, Fuentes A, Magnusson A;
 XX
 DR WPI; 2004-042496/04.

DR N-PSDB; ADF90032.
 XX
 PT New host cell comprising a nucleic acid vector comprising a
 PT cytomegalovirus promoter, an Ig leader sequence, an insert sequence or
 PT SV40 late polyadenylation sequence, useful in producing a chimeric IgE
 PT polypeptide.
 XX
 CC Claim 3; SEQ ID NO 14; 23pp; English.
 XX
 CC The present sequence is the protein sequence of an opossum CH2-human CH3-
 CC opossum CH4 chimeric IgE polypeptide including a C-terminal polyhistidine
 CC sequence (OSO-H). A vector comprising DNA encoding OSO-H can be used for
 CC recombinant production of this chimeric IgE in host, e.g. CHO, cells. The
 CC invention provides methods and materials related to expressing chimeric
 CC IgE proteins. Nucleic acid vectors, host cells, and methods for producing
 CC chimeric IgE polypeptides are provided. When administered to a mammal,
 CC the chimeric polypeptides can reduce the IgE antibody effects of IgE-
 CC related diseases such as asthma, allergies and eczema.
 XX
 SQ Sequence 347 AA;
 CC Query Match 96.2%; Score 1786; DB 8; Length 347;
 CC Best Local Similarity 99.4%; Pred. No. 3.7e-140;
 CC Matches 334; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
 QY 9 TSLSPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTLVVDQGEAE 68
 DB 3 TSLSPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTLVVDQGEAE 62
 QY 69 NLPFYTRPKREGGQTFSLQSEVNI TOGWSSNTYTCHVKHNGSIFEDSSRKCADSNPR 128
 DB 63 NLPFYTRPKREGGQTFSLQSEVNI TOGWSSNTYTCHVKHNGSIFEDSSRKCADSNPR 122
 QY 129 GVSAYLSRSPFDFIRKSPITITCLVVDLAPSKGTVNLWTSRAGKPVNHSTRKEEKORN 188
 DB 123 GVSAYLSRSPFDFIRKSPITITCLVVDLAPSKGTVNLWTSRAGKPVNHSTRKEEKORN 182
 QY 189 GTLVTSTLPVGTREDWIEGTQYCRVTHPLPALMRSTTKL--PGKRLAPEVYMLPPSP 246
 DB 183 GTLVTSTLPVGTREDWIEGTQYCRVTHPLPALMRSTTKL--PGKRLAPEVYMLPPSP 242
 QY 247 EETGTRTRVTCILIRGFYPSISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFLYSRMLV 306
 DB 243 EETGTRTRVTCILIRGFYPSISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFLYSRMLV 302
 QY 307 NKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342
 DB 303 NKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 338

RESULT 5
 ADN00654
 ID ADN00654 standard; protein; 347 AA.
 XX
 AC ADN00654;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE OSO-H protein, SEQ ID 14.
 XX
 KW Antiallergic; Vaccine; self-IgE; ORO; OSO; allergy.
 XX
 OS Synthetic.
 XX
 PN W02004022094-A1.
 XX
 PD 18-MAR-2004.
 XX
 PF 02-JUN-2003; 2003WO-IB003075.
 XX
 PR 05-SEP-2002; 2002US-0408648P.
 XX
 PA (RESI-) RESISTENTIA PHARM AB.

XX Hellman LT, Persson S, Gansson A;
 XX WPI: 2004-248376/23.
 DR N-PSDB; ADN00653.
 XX New composition comprising a self-IgE polypeptide and an aluminum
 PT compound, useful for inducing an anti self-IgE antibody response in a
 PT mammal for treating or preventing allergies.
 XX Claim 3; Fig 16; 102pp; English.
 XX The present invention relates to a composition comprising a polypeptide
 CC and an aluminum compound, where the polypeptide comprises a self-IgE
 CC polypeptide sequence (e.g. an ORO polypeptide or an OSO polypeptide;
 CC ADN00643, ADN00646, ADN00650, ADN00652, ADN00654, ADN00656, ADN00658 or
 CC ADN00661). Administration of the composition to a mammal reduces the
 CC level of detectable free IgE in the mammal. The composition is useful for
 CC inducing an anti self-IgE antibody response in a mammal for treating or
 CC preventing allergies. The present sequence is an OSO protein, used to
 CC illustrate the invention. The OSO-H protein contains an opossum CH2 IgE
 CC domain followed by a human CH3 IgE domain followed by an opossum CH4 IgE
 CC domain. The OSO-H protein also contains a C-terminal polyhistidine tag.
 XX Sequence 347 AA;
 PS Query Match 96.2%; Score 1786; DB 8; Length 347;
 XX Best Local Similarity 99.4%; Pred. No. 3.7e-140;
 CC Matches 334; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
 QY 9 TSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTLVDQGEAE 68
 DB 3 TSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTLVDQGEAE 62
 QY 69 NLPYTRPRKREGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSRKCADSNPR 128
 DB 63 NLPYTRPRKREGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSRKCADSNPR 122
 QY 129 GVSAYLSRSPFDLFRKSTPTICLVVDLAPSKGTNLTWSRAGKPVNHSRKEEKQKN 188
 DB 123 GVSAYLSRSPFDLFRKSTPTICLVVDLAPSKGTNLTWSRAGKPVNHSRKEEKQKN 182
 QY 189 GTLVTSTLPVGRDMEGTGYQCRVTHPLPALMRSTTKL--PGKRLAPEVYMLPPSP 246
 DB 183 GTLVTSTLPVGRDMEGTGYQCRVTHPLPALMRSTTKL--PGKRLAPEVYMLPPSP 242
 QY 247 EETGTTTCLIRGFYPSSEISQVWLFNNEEDTGHHTTTRPKDGHGTDPSPFLYSRLMV 306
 DB 243 EETGTTTCLIRGFYPSSEISQVWLFNNEEDTGHHTTTRPKDGHGTDPSPFLYSRLMV 302
 QY 307 NKSIWEKGNLVTCTRVVHEALPGSRITLKSLSHYSAGN 342
 DB 303 NKSIWEKGNLVTCTRVVHEALPGSRITLKSLSHYSAGN 338
 RESULT 6
 ADF90031
 ID ADF90031 standard; protein; 557 AA.
 XX AC ADF90031;
 XX 26-FEB-2004 (first entry)
 XX Opossum-human chimeric IgE polypeptide.
 XX IgE; immunoglobulin; antibody; opossum; human; vaccine; antiallergic;
 KW antiaesthetic; dermatological; mutant; muten.
 XX Chimeric.
 OS Synthetic.
 OS Didelphis virginiana.
 OS Homo sapiens.
 XX

PN WO2003096966-A2.
 XX 27-NOV-2003.
 XX 15-MAY-2003; 2003WO-IB002503.
 XX 21-MAY-2002; 2002US-0382552P.
 XX (RESI-) RESISTENTIA PHARM AB.
 XX Lundgren M, Fuentes A, Magnusson A;
 XX WPI: 2004-042496/04.
 XX New host cell comprising a nucleic acid vector comprising a
 PT cytomegalovirus promoter, an Ig leader sequence, an insert sequence or
 PT SV40 late polyadenylation sequence, useful in producing a chimeric IgE
 PT polypeptide.
 XX Claim 3; SEQ ID NO 12; 23pp; English.
 XX The present sequence is the protein sequence of an opossum CH2-human CH3-
 CC opoosum CH2-human CH3-opoosum CH4 chimeric IgE polypeptide (modOSO).
 CC The coding sequence for modOSO contains point mutations in the human
 CC CH3 domains that abolish mast cell receptor binding. A vector comprising
 CC DNA encoding modOSO can be used for the recombinant production of the
 CC chimeric IgE in host, e.g. CHO, cells. The invention provides methods and
 CC materials related to expressing chimeric IgE proteins. Nucleic acid
 CC vectors, host cells, and methods for producing chimeric IgE polypeptides
 CC are provided. When administered to a mammal, the chimeric polypeptides
 CC can reduce the IgE antibody effects of IgE-related diseases such as
 CC asthma, allergies and eczema.
 XX Sequence 557 AA;
 PS Query Match 95.5%; Score 1772; DB 8; Length 557;
 XX Best Local Similarity 98.5%; Pred. No. 9.9e-139;
 CC Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 10 LSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTLVDQGEAE 69
 DB 225 IDIPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTLVDQGEAE 284
 QY 70 LFTYTRPRKREGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSRKCADSNPR 129
 DB 285 LFTYTRPRKREGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSRKCADSNPR 344
 QY 130 VSAYLSRSPFDLFRKSTPTICLVVDLAPSKGTNLTWSRAGKPVNHSRKEEKQKN 189
 DB 345 VSAYLSRSPFDLFRKSTPTICLVVDLAPSKGTNLTWSRAGKPVNHSRKEEKQKN 404
 QY 190 TLTVTSTLPVGRDMEGTGYQCRVTHPLPALMRSTTKLPGKRLAPEVYMLPPSP 249
 DB 405 TLTVTSTLPVGRDMEGTGYQCRVTHPLPALMRSTTKLPGKRLAPEVYMLPPSP 464
 QY 250 GTTTRVTCLIRGFYPSSEISQVWLFNNEEDTGHHTTTRPKDGHGTDPSPFLYSRLMV 309
 DB 465 GTTTRVTCLIRGFYPSSEISQVWLFNNEEDTGHHTTTRPKDGHGTDPSPFLYSRLMV 524
 QY 310 IWEKGNLVTCTRVVHEALPGSRITLKSLSHYSAGN 342
 DB 525 IWEKGNLVTCTRVVHEALPGSRITLKSLSHYSAGN 557
 RESULT 7
 ADF90035
 ID ADF90035 standard; protein; 557 AA.
 XX AC ADF90035;
 XX 26-FEB-2004 (first entry)
 XX Opossum-human chimeric IgE polypeptide.
 DE

XX IGE; immunoglobulin; antibody; opossum; human; vaccine; antiallergic;
KW antiasthmatic; dermatological.
XX Chimeric.
OS Digelphis virginiana.
OS Homo sapiens.
XX WO2003096966-A2.
PN 27-NOV-2003.
XX 15-MAY-2003; 2003WO-IB002503.
XX 21-MAY-2002; 2002US-0382552P.
PR (RESI-) RESISTENTIA PHARM AB.
PA Lundgren M, Fuentes A, Magnusson A;
XX WPI: 2004-042496/04.
DR N-PSDB; ADF90034.
XX New host cell comprising a nucleic acid vector comprising a
PT cytomagalovirus promoter, an Ig leader sequence, an insert sequence or
PT SV40 late polyadenylation sequence, useful in producing a chimeric IgE
PT polypeptide.
XX Claim 3; SEQ ID NO 16; 23pp; English.
PS The present sequence is the protein sequence of an opossum CH2-human CH3-
XX opoosum CH2-human CH3-opoosum CH4 (OSOSO) chimeric IgE polypeptide. A
CC vector comprising DNA encoding OSOSO can be used for recombinant
CC production of the chimeric IgE in host, e.g. CHO, cells. The invention
CC provides methods and materials related to expressing chimeric IgE
CC proteins. Nucleic acid vectors, host cells, and methods for producing
CC chimeric IgE polypeptides are provided. When administered to a mammal,
CC the chimeric polypeptides can reduce the IgE antibody effects of IgE-
CC related diseases such as asthma, allergies and eczema.
XX Sequence 557 AA;
SQ
Query Match 95.5%; Score 1772; DB 8; Length 557;
Best Local Similarity 98.5%; Pred. No. 9.9e-139;
Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 10 LSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTVLVDGOEAE 69
Db 225 IDIESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTVLVDGOEAE 284
QY 70 LFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCVKHNGSIFEDSSRKCADSNPRG 129
Db 285 LFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCVKHNGSIFEDSSRKCADSNPRG 344
QY 130 VSAYLSRSPFDLFIKSPITCLVVDLAPSKGTVNLTWASAGKPVNHSRTRKEEKQNG 189
Db 345 VSAYLSRSPFDLFIKSPITCLVVDLAPSKGTVNLTWASAGKPVNHSRTRKEEKQNG 404
QY 190 TLTVTSLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPKRLAPEVYMLPPSPPEET 249
Db 405 TLTVTSLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPKRLAPEVYMLPPSPPEET 464
QY 250 GTTRVTCLIRGFYPSISVQWLFNNEEDTGHHTTTRPKDGHGTDPSPFLYSRMLVNKS 309
Db 465 GTTRVTCLIRGFYPSISVQWLFNNEEDTGHHTTTRPKDGHGTDPSPFLYSRMLVNKS 524
QY 310 IWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
Db 525 IWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 557
RESULT 8
ADN00656

ID ADN00656 standard; protein; 557 AA.
XX AC ADN00656;
XX DT 17-JUN-2004 (first entry)
XX OSOSO protein, SEQ ID 16.
XX Antiallergic; Vaccine; self-IgE; ORO; OSO; allergy.
XX Synthetic.
XX WO2004022094-A1.
XX 19-MAR-2004.
XX 02-JUN-2003; 2003WO-IB003075.
XX 05-SEP-2002; 2002US-0408649P.
XX (RESI-) RESISTENTIA PHARM AB.
XX Hellman LT, Persson S, Gansson A;
XX WPI: 2004-248376/23.
DR N-PSDB; ADN00655.
XX New composition comprising a self-IgE polypeptide and an aluminum
PT compound, useful for inducing an anti self-IgE antibody response in a
PT mammal for treating or preventing allergies.
XX Claim 3; Fig 18; 102pp; English.
XX The present invention relates to a composition comprising a polypeptide
CC and an aluminum compound, where the polypeptide comprises a self-IgE
CC polypeptide sequence (e.g. an ORO polypeptide or an OSO polypeptide;
CC ADN00643, ADN00645, ADN00650, ADN00652, ADN00654, ADN00656, ADN00658 or
CC ADN00661). Administration of the composition to a mammal reduces the
CC level of detectable free IgE in the mammal. The composition is useful for
CC inducing an anti self-IgE antibody response in a mammal for treating or
CC preventing allergies. The present sequence is an OSO protein, used to
CC illustrate the invention. The OSOSO protein contains an opoosum CH2 IgE
CC domain followed by a human CH3 IgE domain followed by an opoosum CH4 IgE
CC domain followed by a human CH3 IgE domain followed by an opoosum CH4 IgE
CC domain.
XX Sequence 557 AA;
SQ
Query Match 95.5%; Score 1772; DB 8; Length 557;
Best Local Similarity 98.5%; Pred. No. 9.9e-139;
Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 10 LSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTVLVDGOEAE 69
Db 225 IDIESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTVLVDGOEAE 284
QY 70 LFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCVKHNGSIFEDSSRKCADSNPRG 129
Db 285 LFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCVKHNGSIFEDSSRKCADSNPRG 344
QY 130 VSAYLSRSPFDLFIKSPITCLVVDLAPSKGTVNLTWASAGKPVNHSRTRKEEKQNG 189
Db 345 VSAYLSRSPFDLFIKSPITCLVVDLAPSKGTVNLTWASAGKPVNHSRTRKEEKQNG 404
QY 190 TLTVTSLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPKRLAPEVYMLPPSPPEET 249
Db 405 TLTVTSLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPKRLAPEVYMLPPSPPEET 464
QY 250 GTTRVTCLIRGFYPSISVQWLFNNEEDTGHHTTTRPKDGHGTDPSPFLYSRMLVNKS 309
Db 465 GTTRVTCLIRGFYPSISVQWLFNNEEDTGHHTTTRPKDGHGTDPSPFLYSRMLVNKS 524
QY 310 IWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342

QY 70 LFPYTRPKRGGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSRKCADSNPRG 129
 Db 285 LFPYTRPKRGGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSRKCADSNPRG 344
 QY 130 VSAVLSRSPSPDLFIRKSPITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQKNG 189
 Db 345 VSAVLSRSPSPDLFIRKSPITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQKNG 404
 QY 190 TLTVTSTLPVGTDRWIEGETYQCRVTHPLPALMRSTTKLPGRKLAPEVYMLPPSPPEET 249
 Db 405 TLTVTSTLPVGTDRWIEGETYQCRVTHPLPALMRSTTKLPGRKLAPEVYMLPPSPPEET 464
 QY 250 GTTRTVTCLIRGFYPSSEISVQWLFNNEEDHTGHHHTTRPKQDKGTDPSPFLYSRMLVNKS 309
 Db 465 GTTRTVTCLIRGFYPSSEISVQWLFNNEEDHTGHHHTTRPKQDKGTDPSPFLYSRMLVNKS 524
 QY 310 IWEKGNLVTQVHVEALPGSRTLEKSLHYSGN 342
 Db 525 IWEKGNLVTQVHVEALPGSRTLEKSLHYSGN 557

RESULT 11

ADP90037 ID ADF90037 standard; protein; 566 AA.

AC ADF90037;

DT 26-FEB-2004 (first entry)

XX Opossum-human chimeric IgE polypeptide.

XX IgE; immunoglobulin; antibody; opossum; human; vaccine; antiallergic;
 XX antiasthmatic; dermatological.

OS Chimeric.

OS Synthetic.

OS Didelphis virginiana.

OS Homo sapiens.

XX WO2003096966-A2.

XX 27-NOV-2003.

XX 15-MAY-2003; 2003WO-IB002503.

XX 21-MAY-2002; 2002US-0382552P.

XX (RESI-) RESISTENTIA PHARM AB.

XX Lundgren M, Fuentes A, Magnusson A;

XX WPI; 2004-042496/04.

XX N-PSDB; ADF90036.

XX New host cell comprising a nucleic acid vector comprising a

PT cytomagalovirus promoter, an Ig leader sequence, an insert sequence or

PT SV40 late polyadenylation sequence, useful in producing a chimeric IgE

XX polypeptide.

XX Claim 3; SEQ ID NO 18; 23pp; English.

XX The present sequence is the protein sequence of an opossum CH2-human CH3-

CC opesum CH2-human CH3-opossum CH4 chimeric IgE polypeptide including a C-

CC terminal polyhistidine sequence (OSOSO-H). A vector comprising DNA

Query Match 95.5%; Score 1772; DB 8; Length 566;
 Best Local Similarity 98.5%; Pred. No.1e-138;
 Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 10 LSLPESGVTIIPPTKVLPHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTVTLVQGEAEN 69
 Db 225 IDIPESGVTIIPPTKVLPHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTVTLVQGEAEN 284
 QY 70 LFPYTRPKRGGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSRKCADSNPRG 129
 Db 285 LFPYTRPKRGGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFEDSSRKCADSNPRG 344
 QY 130 VSAVLSRSPSPDLFIRKSPITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQKNG 189
 Db 345 VSAVLSRSPSPDLFIRKSPITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQKNG 404
 QY 190 TLTVTSTLPVGTDRWIEGETYQCRVTHPLPALMRSTTKLPGRKLAPEVYMLPPSPPEET 249
 Db 405 TLTVTSTLPVGTDRWIEGETYQCRVTHPLPALMRSTTKLPGRKLAPEVYMLPPSPPEET 464
 QY 250 GTTRTVTCLIRGFYPSSEISVQWLFNNEEDHTGHHHTTRPKQDKGTDPSPFLYSRMLVNKS 309
 Db 465 GTTRTVTCLIRGFYPSSEISVQWLFNNEEDHTGHHHTTRPKQDKGTDPSPFLYSRMLVNKS 524
 QY 310 IWEKGNLVTQVHVEALPGSRTLEKSLHYSGN 342
 Db 525 IWEKGNLVTQVHVEALPGSRTLEKSLHYSGN 557

RESULT 12

ADN00658 ID ADN00658 standard; protein; 566 AA.

XX AC ADN00658;

XX 17-JUN-2004 (first entry)

XX OSOSO-H protein, SEQ ID 18.

XX Antiallergic; Vaccine; self-IgE; ORO; OSO; allergy.

XX Synthetic.

XX WO2004022094-A1.

XX 18-MAR-2004.

XX 02-JUN-2003; 2003WO-IB003075.

XX 05-SEP-2002; 2002US-0408648P.

XX (RESI-) RESISTENTIA PHARM AB.

XX Hellman LT, Persson S, Gansson A;

XX WPI; 2004-248376/23.

XX N-PSDB; ADN00657.

XX New composition comprising a self-IgE polypeptide and an aluminum

PT compound, useful for inducing an anti self-IgE antibody response in a

PT mammal for treating or preventing allergies.

XX Claim 3; Fig 20; 102pp; English.

XX The present invention relates to a composition comprising a polypeptide

CC and an aluminum compound, where the polypeptide comprises a self-IgE

CC polypeptide sequence (e.g. an ORO polypeptide or an OSO polypeptide;

CC ADN00643, ADN00646, ADN00650, ADN00652, ADN00654, ADN00656, ADN00658 or
 CC ADN00661). Administration of the composition to a mammal reduces the
 CC level of detectable free IgE in the mammal. The composition is useful for
 CC inducing an anti self-IgE antibody response in a mammal for treating or
 CC preventing allergies. The present sequence is an OSO protein, used to

CC illustrate the invention. The OSO protein contains an opossum CH2 IGE
CC domain followed by a human CH3 IGE domain followed by an opossum CH2 IGE
CC domain followed by a human CH3 IGE domain followed by an opossum CH4 IGE
CC domain. The OSO-H protein also contains a C-terminal polyhistidine tag.
XX
SQ Sequence 566 AA;

Query Match 95.5%; Score 1772; DB 8; Length 566;
Best Local Similarity 98.5%; Pred. No. 1e-138;
Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 LSLPESGPVTIIPTVKLFHSSCDPRGDAHSTTQLCLVSGSPAKVHVTVLVDGQEAEN 69
Db 225 IDIPESGPVTIIPTVKLFHSSCDPRGDAHSTTQLCLVSGSPAKVHVTVLVDGQEAEN 284

QY 70 LFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCHVKNGSIFEDSSRKCADSNPRG 129
Db 285 LFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCHVKNGSIFEDSSRKCADSNPRG 344

QY 130 VSAYLSRPSFPDLFIRKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQKNG 189
Db 345 VSAYLSRPSFPDLFIRKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQKNG 404

QY 190 TLVTSTLPVGTDRWTEGETYQCRVTHPLPALMRSTTKLPCKRLAPEVYMLPPSPPEET 249
Db 405 TLVTSTLPVGTDRWTEGETYQCRVTHPLPALMRSTTKLPCKRLAPEVYMLPPSPPEET 464

QY 250 GTTRVTCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFPLYSRMLVNKS 309
Db 465 GTTRVTCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFPLYSRMLVNKS 524

QY 310 IWEKGNLVCVTVHREALPGSRTLEKSLHYSAGN 342
Db 525 IWEKGNLVCVTVHREALPGSRTLEKSLHYSAGN 557

RESULT 14
ADN00650 standard; protein; 566 AA.
XX
AC ADN00650;
XX
DT 17-JUN-2004 (first entry)
XX
DE modOSO-H protein, SEQ ID 10.
XX
KW Antiallergic; Vaccine; self-IgE; ORO; OSO; allergy.
XX
OS Synthetic.
XX
PN WO2004022094-A1.
XX
PD 18-MAR-2004.
XX
PF 02-JUN-2003; 2003WO-IB003075.
XX
PR 05-SEP-2002; 2002US-0408648P.
XX
PA (RESI-) RESISTENTIA PHARM AB.
XX
PI Hellman LT, Persson S, Gansson A;
XX
DR WPI; 2004-248376/23.
DR N-PSDB; ADN00649.
XX
PT New composition comprising a self-IgE polypeptide and an aluminum
PT compound, useful for inducing an anti self-IgE antibody response in a
PT mammal for treating or preventing allergies.
XX
PS Claim 3; Fig 12; 102pp; English.
XX
CC The present invention relates to a composition comprising a polypeptide
CC and an aluminium compound, where the polypeptide comprises a self-IgE
CC

CC polypeptide sequence (e.g. an ORO polypeptide or an OSO polypeptide:
CC ADN00643, ADN00646, ADN00650, ADN00652, ADN00654, ADN00656, ADN00658 or
CC ADN00661). Administration of the composition to a mammal reduces the
CC level of detectable free IgE in the mammal. The composition is useful for
CC inducing an anti self-IgE antibody response in a mammal for treating or
CC preventing allergies. The present sequence is an OSO protein, used to
CC illustrate the invention. The modOSO-H protein contains an opossum CH2
CC IGE domain followed by a human CH3 IGE domain followed by an opossum CH2
CC IGE domain followed by a human CH3 IGE domain followed by an opossum CH4
CC IGE domain. The modOSO-H protein also contains point mutations in the
CC human CH3 domains that abolish mast cell receptor binding and a C-
XX terminal polyhistidine tag.
SQ Sequence 566 AA;

Query Match 95.5%; Score 1772; DB 8; Length 566;
Best Local Similarity 98.5%; Pred. No. 1e-138;
Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 LSLPESGPVTIIPTVKLFHSSCDPRGDAHSTTQLCLVSGSPAKVHVTVLVDGQEAEN 69
Db 225 IDIPESGPVTIIPTVKLFHSSCDPRGDAHSTTQLCLVSGSPAKVHVTVLVDGQEAEN 284

QY 70 LFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCHVKNGSIFEDSSRKCADSNPRG 129
Db 285 LFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCHVKNGSIFEDSSRKCADSNPRG 344

QY 130 VSAYLSRPSFPDLFIRKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQKNG 189
Db 345 VSAYLSRPSFPDLFIRKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQKNG 404

QY 190 TLVTSTLPVGTDRWTEGETYQCRVTHPLPALMRSTTKLPCKRLAPEVYMLPPSPPEET 249
Db 405 TLVTSTLPVGTDRWTEGETYQCRVTHPLPALMRSTTKLPCKRLAPEVYMLPPSPPEET 464

QY 250 GTTRVTCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFPLYSRMLVNKS 309
Db 465 GTTRVTCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKQKHGTDPSFPLYSRMLVNKS 524

QY 310 IWEKGNLVCVTVHREALPGSRTLEKSLHYSAGN 342
Db 525 IWEKGNLVCVTVHREALPGSRTLEKSLHYSAGN 557

RESULT 14
ADN00661 standard; protein; 353 AA.
XX
AC ADN00661;
XX
DT 17-JUN-2004 (first entry)
XX
DE H-OCO-H protein, SEQ ID 21.
XX
KW Antiallergic; Vaccine; self-IgE; ORO; OSO; allergy.
XX
OS Synthetic.
XX
PN WO2004022094-A1.
XX
PD 18-MAR-2004.
XX
PF 02-JUN-2003; 2003WO-IB003075.
XX
PR 05-SEP-2002; 2002US-0408648P.
XX
PA (RESI-) RESISTENTIA PHARM AB.
XX
PI Hellman LT, Persson S, Gansson A;
XX
DR WPI; 2004-248376/23.
DR N-PSDB; ADN00660.
XX

PT New composition comprising a self-IgE polypeptide and an aluminum
 PR compound, useful for inducing an anti self-IgE antibody response in a
 PR mammal for treating or preventing allergies.

XX Claim 3; Fig 23; 102pp; English.

XX The present invention relates to a composition comprising a polypeptide
 CC and an aluminum compound, where the polypeptide comprises a self-IgE
 CC polypeptide sequence (e.g. an ORO polypeptide or an OSO polypeptide:
 CC ADN00643, ADN00646, ADN00650, ADN00652, ADN00654, ADN00656, ADN00658 or
 CC ADN00661). Administration of the composition to a mammal reduces the
 CC level of detectable free IgE in the mammal. The composition is useful for
 CC inducing an anti self-IgE antibody response in a mammal for treating or
 CC preventing allergies. The present sequence is H-OCO-H protein, used to
 CC illustrate the invention. The H-OCO-H protein contains an opossum CH2 IgE
 CC domain followed by a monkey CH3 IgE domain followed by an opossum CH4 IgE
 CC domain. The H-OCO-H protein also contains a N- and C-terminal
 CC polyhistidine tags.

XX Sequence 353 AA;

Query Match 94.8%; Score 1759; DB 8; Length 353;
 Best Local Similarity 95.3%; Pred. No. 6,7e-138;
 Matches 328; Conservative 3; Mismatches 11; Indels 2; Gaps 1;

QY 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60
 DB 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60
 QY 61 LVDGQEAENLPYTRPRKREGGQTFSLQSEVNTTQGWMSNTYTCHVXNGSIFEDSSR 120
 DB 61 LVDGQEAENLPYTRPRKREGGQTFSLQSEVNTTQGWMSNTYTCHVXNGSIFEDSSR 120
 QY 121 KCADSNPRGVSAYLSRSPDLFIRKSPITICLVVDLAPSKGTVNLTWASRSGKPVNHST 180
 DB 121 KCADSNPRGVSAYLSRSPDLFIRKSPITICLVVDLAPSKGTVNLTWASRSGKPVNHST 180
 QY 181 RKEEKQKNGTLTSTLPVGTTRDWIEGETYQCRVTHPHLPALMRSTTKL--PGKRLAPE 238
 DB 181 ATGKKQKNGTLTSTLPVGTTRDWIEGETYQCRVTHPHLPALMRSTTKL--PGKRLAPE 240
 QY 239 VYMLPPSPETGTRTRVTCLIRGFYPSSEISVQWLFNNEEDHTGHHTTTPQKHGTDPSF 298
 DB 241 VYMLPPSPETGTRTRVTCLIRGFYPSSEISVQWLFNNEEDHTGHHTTTPQKHGTDPSF 300
 QY 299 FLYSRMLVNKSIWEKGNLVCRCVVHEALPGSRITLKSLSHYSAGN 342
 DB 301 FLYSRMLVNKSIWEKGNLVCRCVVHEALPGSRITLKSLSHYSAGN 344

RESULT 15

AAB06208
 ID AAB06208 standard; protein; 341 AA.

XX AC AAB06208;

XX DT 12-SEP-2003 (revised)

XX DT 22-NOV-2000 (first entry)

XX Immunogenic peptide consisting of opossum CH2, dog CH3 and opossum CH4.
 DE Dog; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;
 KW asthma; eczema; immunogenic peptide.

XX Didelphis virginiana.

OS Canis sp.

OS Chimeric.

XX WO200025722-A2.

XX 11-MAY-2000.

XX 21-OCT-1999; 99WO-SE001896.

XX 02-NOV-1998; 98US-0106652P.
 PR 22-SEP-1999; 98US-00401636.
 XX (RESI-) RESISTENTIA PHARM AB.

XX Hellman LT;

XX WPI; 2000-365342/31.

XX Immunogenic polypeptides useful for preventing the harmful effects of
 PR immunoglobulin E in mammals.

XX Disclosure; Fig 2; 50pp; English.

XX The present sequence is an immunogenic peptide consisting of the heavy
 CC chain constant regions 2 and 4 of the opossum IgE and the heavy chain
 CC constant region 3 from the dog. It was shown to cause a stronger
 CC polyclonal anti-self IgE response than peptides consisting of the same
 CC regions from one mammal. Immunogenic peptides, particularly those
 CC consisting of different heavy chain constant regions, can be used for
 CC vaccination in humans, against bacterial and viral infections and
 CC allergies, such as asthma, fur, pollen and food allergies and eczema.
 CC (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 341 AA;

Query Match 88.6%; Score 1644.5; DB 3; Length 341;
 Best Local Similarity 88.0%; Pred. No. 2.2e-128;
 Matches 301; Conservative 17; Mismatches 23; Indels 1; Gaps 1;

QY 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60
 DB 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTV 60
 QY 61 LVDGQEAENLPYTRPRKREGGQTFSLQSEVNTTQGWMSNTYTCHVXNGSIFEDSSR 120
 DB 61 LVDGQEAENLPYTRPRKREGGQTFSLQSEVNTTQGWMSNTYTCHVXNGSIFEDSSR 120
 QY 121 KCADSNPRGVSAYLSRSPDLFIRKSPITICLVVDLAPSKGTVNLTWASRSGKPVNHST 180
 DB 121 KCSESDPRGVTSYLSPPSPDLTYVHKAPKITCLVVDLATWEG-MNLTWYRESKEPVNPGP 179
 QY 181 RKEEKQKNGTLTSTLPVGTTRDWIEGETYQCRVTHPHLPALMRSTTKLPGKRLAPEVY 240
 DB 180 LNKXDFHNGTITVTSTLPVNTNDWIEGETYCYRVTHPHLPKDIVRSIAKLPGKRLAPEVY 239
 QY 241 MLPPSPETGTRTRVTCLIRGFYPSSEISVQWLFNNEEDHTGHHTTTPQKHGTDPSF 300
 DB 240 MLPPSPETGTRTRVTCLIRGFYPSSEISVQWLFNNEEDHTGHHTTTPQKHGTDPSF 299
 QY 301 YSRMLVNKSIWEKGNLVCRCVVHEALPGSRITLKSLSHYSAGN 342
 DB 300 YSRMLVNKSIWEKGNLVCRCVVHEALPGSRITLKSLSHYSAGN 341

Search completed: November 14, 2004, 14:58:12

Job time : 167 secs

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29	407.5	22.0	326	4	US-09-467-638-3	Sequence 3, Appli
30	407.5	22.0	328	3	US-08-808-720-1	Sequence 1, Appli
31	407.5	22.0	328	4	US-09-467-638-1	Sequence 1, Appli
32	407.5	22.0	331	3	US-08-808-720-5	Sequence 5, Appli
33	407.5	22.0	331	4	US-09-467-638-5	Sequence 5, Appli
34	406	21.9	309	4	US-09-883-777-7	Sequence 7, Appli
35	405.5	21.8	218	4	US-09-483-588-3	Sequence 3, Appli
36	404.5	21.8	218	4	US-09-483-588-6	Sequence 6, Appli
37	404.5	21.8	247	4	US-09-428-082B-12	Sequence 12, Appli
38	404.5	21.8	269	4	US-09-428-082B-10	Sequence 10, Appli
39	404	21.8	252	4	US-09-428-082B-1066	Sequence 1066, Ap
40	404	21.8	300	4	US-09-883-777-9	Sequence 9, Appli
41	404	21.8	331	3	US-09-178-869-2	Sequence 2, Appli
42	404	21.8	331	4	US-09-761-413-2	Sequence 2, Appli
43	403.5	21.7	248	4	US-09-428-082B-1062	Sequence 1062, Ap
44	403	21.7	281	4	US-09-854-864-10	Sequence 10, Appli
45	402.5	21.7	218	4	US-09-483-588-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-232-539D-56
; Sequence 56, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardiou, Paula M.
; TITLE OF INVENTION: Ige Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232.539D
; FILING DATE: 21-Apr-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-232-539D-56

Query Match 31.2%; Score 579; DB 2; Length 113;
Best Local Similarity 98.2%; Pred. No. 1.3e-48;
Matches 109; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 122 CADSNPRGVSAVLSRPSFDLIRKSPITCLVVDLPASKGTNLVWSRSGKPNVHSTR 161

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OM protein - protein search, using sw model
Run on: November 14, 2004, 15:03:41 ; Search time 24 Seconds
(without alignments)
945.032 Million cell updates/sec
Title: US-09-401-636-8
Perfect score: 1856
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 417130
Minimum DB seq length: 0
Maximum DB seq length: 342
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	579	31.2	113	2	US-08-232-539D-56
2	548.5	29.6	109	3	US-08-466-163B-1
3	548.5	29.6	109	4	US-09-802-096-1
4	548.5	29.6	109	4	US-09-802-077-1
5	538	29.0	106	2	US-08-232-539D-54
6	512	27.6	334	2	US-08-646-981-16
7	508	27.4	119	2	US-08-464-025A-1
8	501.5	27.0	331	2	US-08-646-981-17
9	490.5	26.4	118	3	US-08-466-151-1
10	490	26.4	333	1	US-08-436-463-6
11	490	26.4	333	1	US-08-024-253-6
12	476.5	25.7	329	4	US-09-313-942-12
13	476	25.6	327	2	US-08-761-277A-47
14	475.5	25.6	326	2	US-08-656-586-9
15	457	24.6	330	2	US-09-301-593-22
16	434	23.4	320	2	US-08-579-940-8
17	421.5	22.7	331	3	US-08-808-720-7
18	421.5	22.7	331	3	US-09-467-638-7
19	415.5	22.4	324	2	US-08-579-940-7
20	414	22.3	228	4	US-09-968-362A-27
21	411.5	22.2	218	4	US-09-483-588-7
22	411.5	22.2	229	4	US-09-968-362A-28
23	411.5	22.2	277	4	US-09-428-082B-20
24	411	22.1	253	4	US-09-428-082B-18
25	409	22.0	313	3	US-08-713-558F-36
26	408.5	22.0	217	4	US-09-483-588-5
27	408.5	22.0	283	4	US-09-854-864-9

Db 1 CADSNPRGVSAYLSRSPFDLFIKSPPTITCLVVDLAPSKGTNLTWSRASKPNNHSTR 60
Qy 182 KEKQKNGTLTVTSTLPGVTRDWIEGETYQCRVTHPHLPRALMRSTTKLPG 232
Db 61 KEKQKNGTLTVTSTLPGVTRDWIEGETYQCRVTHPHLPRALMRSTTKTSG 111

RESULT 2

US-08-466-163B-1
; Sequence 1, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 1
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-466-163B-1

Query Match 29.6%; Score 548.5; DB 3; Length 109;
Best Local Similarity 97.2%; Pred. No. 1.1e-45;
Matches 106; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
Qy 124 DSNPRGVSAYLSRSPFDLFIKSPPTITCLVVDLAPSKGTNLTWSRASKPNNHSTRKE 183
Db 1 DSNPRGVSAYLSRSPFDLFIKSPPTITCLVVDLAPSKGTNLTWSRASKPNNHSTRKE 60
Qy 184 EKQKNGTLTVTSTLPGVTRDWIEGETYQCRVTHPHLPRALMRSTTKLPG 232
Db 61 EKQKNGTLTVTSTLPGVTRDWIEGETYQCRVTHPHLPRALMRSTTKTSG 108

RESULT 3

US-09-802-096-1
; Sequence 1, Application US/09802096
; Patent No. 6685939
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 1
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-802-096-1

Query Match 29.6%; Score 548.5; DB 4; Length 109;
Best Local Similarity 97.2%; Pred. No. 1.1e-45;
Matches 106; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
Qy 124 DSNPRGVSAYLSRSPFDLFIKSPPTITCLVVDLAPSKGTNLTWSRASKPNNHSTRKE 183
Db 1 DSNPRGVSAYLSRSPFDLFIKSPPTITCLVVDLAPSKGTNLTWSRASKPNNHSTRKE 60
Qy 184 EKQKNGTLTVTSTLPGVTRDWIEGETYQCRVTHPHLPRALMRSTTKLPG 232
Db 61 EKQKNGTLTVTSTLPGVTRDWIEGETYQCRVTHPHLPRALMRSTTKTSG 108

RESULT 4

US-09-802-077-1
; Sequence 1, Application US/09802077
; Patent No. 6699472
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 1
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-077-1

Query Match 29.6%; Score 548.5; DB 4; Length 109;
Best Local Similarity 97.2%; Pred. No. 1.1e-45;
Matches 106; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
Qy 124 DSNPRGVSAYLSRSPFDLFIKSPPTITCLVVDLAPSKGTNLTWSRASKPNNHSTRKE 183
Db 1 DSNPRGVSAYLSRSPFDLFIKSPPTITCLVVDLAPSKGTNLTWSRASKPNNHSTRKE 60
Qy 184 EKQKNGTLTVTSTLPGVTRDWIEGETYQCRVTHPHLPRALMRSTTKLPG 232
Db 61 EKQKNGTLTVTSTLPGVTRDWIEGETYQCRVTHPHLPRALMRSTTKTSG 108

RESULT 5

US-08-232-539D-54
; Sequence 54, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: IGE Antagonists
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,539D
FILING DATE: 21-Apr-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/178583
FILING DATE: 07-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-232-539D-54

Query Match 29.0%; Score 538; DB 2; Length 106;
Best Local Similarity 98.1%; Pred. No. 1.1e-44;
Matches 102; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 129 GVSAYLSRSPDLFRKSPPTICLVVDLAPSKGTNLTWSRSGKPVNHSRKEEKORN 188
DB 1 GVSAYLSRSPDLFRKSPPTICLVVDLAPSKGTNLTWSRSGKPVNHSRKEEKORN 60

QY 189 GTLVTSTLPVGRDWEIEGYQCRVTHPLRALMRSTTKLPF 232
DB 61 GTLVTSTLPVGRDWEIEGYQCRVTHPLRALMRSTTKTSG 104

RESULT 6
US-08-646-981-16
Sequence 16, Application US/08646981
Patent No. 5852183
GENERAL INFORMATION:
APPLICANT: MAEDA, HIROAKI
APPLICANT: KAWACHI, KAZUHIKO
APPLICANT: ONO, YOICHI
APPLICANT: TOKIYOSHI, SACHIO
TITLE OF INVENTION: DOG-MOUSE HETEROHYBRIDOMA AND GENE
TITLE OF INVENTION: FRAGMENT CODING FOR CONSTANT REGION OF CANINE
TITLE OF INVENTION: IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,981
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S

Query Match 27.6%; Score 512; DB 2; Length 334;
Best Local Similarity 35.9%; Pred. No. 2.1e-41;
Matches 123; Conservative 60; Mismatches 122; Indels 38; Gaps 12;

QY 23 PTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW-----LVDGOEAEENLPYTRPK 78
DB 5 PSVFPLDPSCG--STSGSTVALACLVSQYFPEPVTVMNSGSLTSG-----VHTFPDS 55

QY 79 REGQTFESLOSEYNIQTQOMSSNTYCHVKH-----NGSIFE--DSSRK 121
DB 56 LQSSGLYSLSMVTVPSSRW-SSETFTCNVAHPASKTKVDKPVKRENGRVPRPPDCPKC 114

QY 122 CADSNPRGVSAYLSRSPFD-LFIRKSPPTICLVVDLAPSKGTNLTWSRSGKPVNHS- 179
DB 115 PAPEMLGGPSVFIPPPKPKDTLLIARTPEVTCVVVDLGPEDPEVQISWF-VDGKQMOTAK 173

QY 180 TRKEEKORNGTLVTSTLPVGRDWEIEGYQCRVTHPLRALMRSTTKLPKRLAPEV 239
DB 174 TOPREDFNGYRVVSVLPDIGHQDLKQFTKVNKALPSPRIETISKARGOAHQPSV 233

QY 240 YMLPPSPPEE-TGTRTIVTCLIRGYPSEISVQMLFNNEEDHTGHTTTRQKHGTDPSP 298
DB 234 YVLPSPREELSKNTVSLTKIDFPDIDVEMQSQBPESKYRTTPQLDE--DGSY 291

QY 299 FLYERMLVNSIKWKNLVTCAVWHEALPGSRITLESLSHYSA 341
DB 292 FLYSKLSYDKSRWQRGDTFFICAVMHEALHNYT-QKSLSHSPG 333

RESULT 7
US-08-464-025A-1
Sequence 1, Application US/08464025A
Patent No. 5994514
GENERAL INFORMATION:
APPLICANT: Jardieu et al.
TITLE OF INVENTION: IMMUNOGLOBULIN VARIANTS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,025A
FILING DATE: 05-Jun-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-464-025A-1

Query Match 27.4%; Score 508; DB 2; Length 119;
 Best Local Similarity 88.9%; Pred. No. 1.1e-41;
 Matches 104; Conservative 1; Mismatches 4; Indels 8; Gaps 4;
 QY 124 DSNPRGVSAYLSRSPD-LFIRKSPITITCLVVDLAPSKGTNLTWSRAS---GKPVNHS 179
 DB 2 DSNPRGVSAYLSRSPD-LFIRKSPITITCLVVDLAPSKGTNLTWSRASXXGKPVNHS 61
 QY 180 TRKEEKOR---NGHLTVSTLPGVTRDWIEGTYQCRVTHPHLPRAL-MRSTTKLFG 232
 DB 62 TRKEEKORXXXGTLTVSTLPGVTRDWIEGTYQCRVTHPHLPRALXMRSTTKTSG 118

RESULT 8

US-08-646-981-17
 ; Sequence 17, Application US/08646981
 ; Patent No. 5852183
 ; GENERAL INFORMATION:
 ; APPLICANT: MAEDA, HIRAKAI
 ; APPLICANT: ED, YASUYUKI
 ; APPLICANT: KIMACHI, KAZUHIKO
 ; APPLICANT: ONO, YOICHI
 ; APPLICANT: TOKIYOSHI, SACHIO
 ; TITLE OF INVENTION: DOG-MOUSE HETEROHYBRIDOMA AND GENE
 ; TITLE OF INVENTION: FRAGMENT CODING FOR CONSTANT REGION OF CANINE
 ; TITLE OF INVENTION: IMMUNOGLOBULINS
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
 ; STREET: PO BOX 747
 ; CITY: FALLS CHURCH
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22040-0747
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/646,981
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WEINER, MARC S
 ; REGISTRATION NUMBER: 32,181
 ; REFERENCE/DOCKET NUMBER: 1488-106
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 331 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-646-981-17

Query Match 27.0%; Score 501.5; DB 2; Length 331;
 Best Local Similarity 36.3%; Pred. No. 2.2e-40;
 Matches 122; Conservative 62; Mismatches 125; Indels 27; Gaps 12;
 QY 23 PTVKLFHSSCDPRGDAHSTIQLLVSGFSAKVHTVWLVDGQAEANLFPVTPRKREGG 82
 DB 5 PSVFPLAPSCG--STSGSTVTLACLVSQGFPEPVTVM-NSGSLTSGVHTFSPVLKSG- 60
 QY 83 QTFSLQSEWNITQGWMSNNTVCHVKNGS-----IFDSRRKCADSNP-----RG 129
 DB 61 -LYLSLSSMVTPESSR-LPSETFTCNVHPATNTKVDKFGVPKSTCKICISPCVPESLIG 118

QY 130 VSAVLSRSPDLE-IRKSPITITCLVVDLAPSKGTNLTWSRASGKPVNHS-TRKEEKOR 187
 DB 119 PSVFIFPPFKDILIRITPPTVTCVLDLGRDEVOISWF-VDCKEVHTAKTQPRQOF 177
 QY 188 NGTLTVSTLPGVTRDWIEGTYQCRVTHPHLPRALMRSTTKLPGKSLADEVYMLPSPPE 247
 DB 178 NSTYRVVSVLPTEHQDMLTKGPKRCRVNHHGLPSPPIERTISKARGQAHPGVVLPSPK 237
 QY 248 E--TGCTTETVTCCLIRGVFVPSISVQWLFNNEEDHTGHTTTRPKOKHGTDPSPFLYSRML 305
 DB 238 ELSGSDVTLLCLIKDFPPEIDVWQSNQGPPEPSKYHTTAPOLDE--DGSVFLYSKLS 295
 QY 306 VNSIWEKGNLVTCRVVHEALPGSRITLKSLSHYSAG 341
 DB 296 VDKSRWEQGDPTCAVMHEALQNHYT-DLSLSHSPG 330

RESULT 9

US-08-466-151-1
 ; Sequence 1, Application US/08466151
 ; Patent No. 6037453
 ; GENERAL INFORMATION:
 ; APPLICANT: Jardiou, Paula M.
 ; APPLICANT: Presta, Leonard G.
 ; TITLE OF INVENTION: Immunoglobulin Variants
 ; NUMBER OF SEQUENCES: 65
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Winpatin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/466,151
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/466163
 ; FILING DATE: 06-Jun-1995
 ; APPLICATION NUMBER: 08/405617
 ; FILING DATE: 15-MAR-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/185899
 ; FILING DATE: 26-JAN-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/879495
 ; FILING DATE: 07-MAY-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/744768
 ; FILING DATE: 14-AUG-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Svoboda, Craig G.
 ; REGISTRATION NUMBER: 39,044
 ; REFERENCE/DOCKET NUMBER: P07182PCID1
 ; TELEPHONE: 650/225-1489
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 118 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; US-08-466-151-1

Query Match 26.4%; Score 490.5; DB 3; Length 118;
 Best Local Similarity 88.0%; Pred. No. 5.5e-40;
 Matches 103; Conservative 1; Mismatches 4; Indels 9; Gaps 5;

QY 124 DSNPRGVSAYLGRSPFD-LFIRKPTTCLVVDLAPSKGTNLWTSRAS---GKPVNHS 179
 Db 2 DSNPRGVSAYLGRSPFDLFIKSPITITCLVVDLAPSKGTNLWTSRASXXGKPVNHS 61
 QY 180 TRKEEQR--NGTLTVTSTLPVGRDWDIEGETYQCRVTHPLRAL-MRSTTKLPG 232
 Db 62 TRKEEQRXXXGTLTSTLPVGRDWDIEGET-QCRVTHPLRALXWRSTTKTSG 117

RESULT 10
 US-08-436-463-6
 ; Sequence 6, Application US/08436463
 ; Patent No. 5760185
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMACHI, Kazuhiko
 ; APPLICANT: MAEDA, Hiroaki
 ; APPLICANT: NISHIYAMA, Kiyoto
 ; APPLICANT: TOKIYOSHI, Sachio
 ; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
 ; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
 ; STREET: 419 Seventh Street, N.W., Suite 400
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA: US/08/436,463
 ; APPLICATION NUMBER: 37,971
 ; FILING DATE: 26-JUN-1995
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 341255/1992
 ; FILING DATE: 28-NOV-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: YUN, Allen C.
 ; REGISTRATION NUMBER: 37,971
 ; REFERENCE/DOCKET NUMBER: KIMACHI=1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 333 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-436-463-6

Query Match 26.4%; Score 490; DB 1; Length 333;
 Best Local Similarity 34.2%; Pred. No. 2.9e-39;
 Matches 117; Conservative 63; Mismatches 126; Indels 36; Gaps 12;
 QY 23 PTVKLFHSCDPRGDAHSTIQLCLVSGFSPAKVHVW---LVDGQEAENLFPYTRPK 78
 Db 4 PSVFFPLAPSCGTTSGA--TVALACLVLGYFFPEPTVSVNSGALTSG---VHTFPAVL--- 55
 QY 79 REGGQTFSLQSEVNITQGMSSNTYTCVVKH--NGSIFEDSSRK-----CADS 125
 Db 56 -QASGLYSLSMVTPSSRWL--SDTFCNVAHPSPNTKVDKTRKTDHPGPKPCDCPKC 113
 QY 126 NP-----RGVSAYLGRSPFD-LFIRKPTTCLVVDLAPSKGTNLWTSRASGKPVNHS 180
 Db 114 PPEMLGSPSIFIFPPKPTLSISRTPEVTCCLVVDLGDSDVDQITFVNDVQVYTAKT 173
 QY 181 RKEEQRNGTLTSTLPVGRDWDIEGETYQCRVTHPLRALMRSTTKLPGKRLAPEVY 240

Db 174 SPREEQNSYRVVSVLPILHQLWLGKPKCKVNSKSLSPERTISAKGQPHBPQVY 233
 QY 241 MLPPSPETGTR-TVTCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKDGHGTPSPF 299
 Db 234 VLPPAQBELSRNKSVTCLIKSFHPDIAVEMITQOPEPENNYRTTPQLD--SGTYF 291
 QY 300 LYSMLVYKNSIWEKGNLAVTCRVVHEALPGSRITLKSLSHSAG 341
 Db 292 VYSKLSVDRSHWQGNNTYTCVSHEALHSHHT-QKSLTQSPG 332

RESULT 11
 US-08-024-253-6
 ; Sequence 6, Application US/08024253
 ; Patent No. 5785968
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMACHI, Kazuhiko
 ; APPLICANT: MAEDA, Hiroaki
 ; APPLICANT: NISHIYAMA, Kiyoto
 ; APPLICANT: TOKIYOSHI, Sachio
 ; APPLICANT: TOHYA, Yukinobu
 ; APPLICANT: MIKAMI, Takeshi
 ; TITLE OF INVENTION: ANTI-FELINE CALCIVIRUS RECOMBINANT
 ; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT ENCODING THE SAME
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: WEGNER, CANTOR, MUELLER & PLAYER
 ; STREET: 1233 20th Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20036-8218
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/024,253
 ; FILING DATE: 19930301
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 79189/1992
 ; FILING DATE: 28-FEB-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: CANTOR, Herbert I.
 ; REGISTRATION NUMBER: 24,392
 ; REFERENCE/DOCKET NUMBER: P-500-23744
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 887-0400
 ; TELEFAX: (202) 835-0605
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 333 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-024-253-6

Query Match 26.4%; Score 490; DB 1; Length 333;
 Best Local Similarity 34.2%; Pred. No. 2.9e-39;
 Matches 117; Conservative 63; Mismatches 126; Indels 36; Gaps 12;
 QY 23 PTVKLFHSCDPRGDAHSTIQLCLVSGFSPAKVHVW---LVDGQEAENLFPYTRPK 78
 Db 4 PSVFFPLAPSCGTTSGA--TVALACLVLGYFFPEPTVSVNSGALTSG---VHTFPAVL--- 55
 QY 79 REGGQTFSLQSEVNITQGMSSNTYTCVVKH--NGSIFEDSSRK-----CADS 125
 Db 56 -QASGLYSLSMVTPSSRWL--SDTFCNVAHPSPNTKVDKTRKTDHPGPKPCDCPKC 113

QY 126 NP---RVSAYLGRSPFD-LFIRKSPITICLVVDLAPSKGTVNLWTSRASKPVNHS 180
DB 114 PPMELGSPSIFIPPKPKTSLSRPEVTCVVDLGPDDSDVQITFWVDNTQVYAKT 173
QY 181 RKEKQRNGTLVTVSTLPGVTRDWEGETYQCRVTHPLPRALMRSTTKLPGRKLAPEVY 240
DB 174 SPREEQFNSTVRVSVLPILHODWLGKFKCKVNSKSLPSPIERTISAKAGQHPQVY 233
QY 241 MLPSPBETGTR-TVTCIRGFPVPSISVQWLFNNEEDHTGHTTTRPKQKHGTDPSP 299
DB 234 VLPQAEBSLNKSVTVCLIKSFHPPDIAVEWITGOPEPNRYTTPQLD--SDGTIF 291
QY 300 LYSRLVYNKSWKGNLTVCRVHEALPGSRTLEKSLHSAG 341
DB 292 VYSLVDRSHWQGNNTYTCVSHEALHSHT-QKSLTQSPG 332

RESULT 12

US-09-313-942-12
; Sequence 12, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT FILING DATE: 1999-05-19
; PRIOR FILING DATE: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-12

Query Match 25.7%; Score 476.5; DB 4; Length 329;
Best Local Similarity 35.5%; Pred. No. 5.8e-38;
Matches 122; Conservative 58; Mismatches 131; Indels 33; Gaps 12;
QY 15 SGPTIIPPTVKLFHSCDPRGDAHSTIQLCLVSGFSPAKVHTV---LVDGQAEHL 70
DB 1 SGATKGPSVFPL--APCS-RSTSESTAALGCLVKDYFPEPTVSNWNSGALTSG--VHT 54
QY 71 FVYTRPKREGGQTFSLQGEVNTIQGMSSNTYTCHVKHNGSIFEDSSRKCADSNP--- 127
DB 55 FPAVL---QSSGLYSLSSVTVFSSS-LGKTYTCNVDEKPSNTKVDKVESKYGPFCP 109
QY 128 -----RGVSAYLGRSPFD-LFIRKSPITICLVVDLAPSKGTVNLWTSRASKPVN 178
DB 110 SCPAPFLGSPSVFLFPKPKTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVNA 169
QY 179 STRKEKQRNGTLVTVSTLPGVTRDWEGETYQCRVTHPLPRALMRSTTKLPGRKLAPE 238
DB 170 KTKPREQFNSTVRVSVLPILHODWLGKFKCKVNSKSLPSPIERTISAKAGQHPQVY 229
QY 239 VYMLPSPBETGTR-TVTCIRGFPVPSISVQWLFNNEEDHTGHTTTRPKQKHGTDPSP 297
DB 230 VYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQEN--NYKTTTPVLD--SDGS 285
QY 298 FFLYSRLVYNKSWKGNLTVCRVHEALPGSRTLEKSLHSAG 341
DB 286 FFLYSRLTVDKSRWQGNVFCVSWHEALHNYT-QKSLUSL 328

RESULT 13

US-08-761-277A-47
; Sequence 47, Application US/08761277A
; Patent No. 5972334

; GENERAL INFORMATION:
; APPLICANT: Denney Jr., Dan W.
; TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And
; NUMBER OF INVENTIONS: Leukemia
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,277A
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/644,664
; FILING DATE: 01-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: GENITOP-02406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 327 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-761-277A-47

Query Match 25.6%; Score 476; DB 2; Length 327;
Best Local Similarity 35.8%; Pred. No. 6.5e-38;
Matches 116; Conservative 57; Mismatches 121; Indels 30; Gaps 10;
QY 35 RGDHSTIQLCLVSGFSPAKVHTV---LVDGQAEHLFPYTRPKREGGQTFSLQSE 90
DB 16 RSTSESTAALGCLVKDYFPEPTVSNWNSGALTSG--VHTFPAVL---QSSGLYSLSSV 68
QY 91 VNTIQGMSSNTYTCHVKHNGSIFEDSSRKCADSNP-----RGVSAYLGRSP 139
DB 69 VTFPSSS-LGKTYTCNVDEKPSNTKVDKVESKYGPFCPAPFLGSPVFLFPK 127
QY 140 FD-LFIRKSPITICLVVDLAPSKGTVNLWTSRASKPVNHSRKEKQRNGTLVTVSTLP 198
DB 128 KDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVNAKTPREEQFNSTVRVSVLT 187
QY 199 VGRDTEGETYQCRVTHPLPRALMRSTTKLPGRKLAPEVYMLPSPBETGTR-TVTC 257
DB 188 VLHQDWLNGKEYCKVKNSKSLPSPIERTISAKAGQHPQVYTLPPSQEEMTKNQVSLT 247
QY 258 LIRGFYPSISVQWLFNNEEDHTGHTTTRPKQKHGTDPSPFLYSRLVYNKSWKGNL 317
DB 248 LVKGFYPSDIAVEWESNGQEN--NYKTTTPVLD--SDGSFFLYSLTVDKSRWQGNV 303
QY 318 TCRVHEALPGSRTLEKSLHSAG 341
DB 304 SCSVMHEALHNYT-QKSLUSL 326

RESULT 14

US-08-656-586-9
; Sequence 9, Application US/08656586
; Patent No. 5834597
; GENERAL INFORMATION:

```

; APPLICANT: Tso, J. Yun
; APPLICANT: Cole, Michael S.
; APPLICANT: Anasetti, Claudio
; TITLE OF INVENTION: Mutated No. 5834597activating IgG2 Domains and
; TITLE OF INVENTION: Anti-CD3 Antibodies Incorporating the Same
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/656,586
; FILING DATE: 31-MAY-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joseph O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-007210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 326 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..326
; OTHER INFORMATION: /note= "heavy chain constant region of
; OTHER INFORMATION: IgG2 mutant 3"
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; US-08-656-586-9
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; Query Match 25.6%; Score 475.5; DB 2; Length 326;
; Best Local Similarity 35.8%; Pred. No. 7.2e-38;
; Matches 115; Conservative 57; Mismatches 120; Indels 29; Gaps 11;
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; QY 35 RGAHSTIQLCLVSGSPAKVHTW---LVDGQEAENLFPYTRPKREGGQTSLOSE 90
; DB 16 RSTSESTAALGCLVKDYFPEPTVSNWNSGALTSG---VHTFPAVL---QSSGLYSLSV 68
; QY 91 VNITQGWMSNTYTCVHGH---NGSIFEDSRKCADSNP-----RGVSAYLSRPSPF 140
; DB 69 VTPVSSNF-GTQVTCNVHDKPSNTKVDKTVKCKCCVCPPCPAPPAAAPSVLFPKPK 127
; QY 141 D-LFIRKSPITCLVLDLAPSKGTVALTWSRASKPVNHSRSTKEKQKNGTLTSTLPV 199
; DB 128 DTLMSITPEVTCVVDVSHDEDEVQPNVYDGVGVHNAKTKPREQFNSTFRVSVLIV 187
; QY 200 GTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGRKLAPEVYMLPPSPPEE-TGTRVTCL 258
; DB 188 VHQDLNGKEYCKVSKNGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCL 247
; QY 259 IRGYPSEISVQWLFNNEEDHTGHTTRPKQKHGTDTPSFYLSRMLVNSIWEKGNLVT 318
; DB 248 VKGFYPSDIAVWESNQOPEN--NYKTPPMLD--SDGSFFLYSKLTVDKSRQQGVFS 303
; QY 319 CRVVHEALPGSRTLEKSLIHS 339
; DB 304 CSNVHEALHNHYT-QKSLSL 323
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; RESULT 15
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; US-09-301-593-22
; Sequence 22, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: PAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 6652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 22
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
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; US-09-301-593-22
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; Query Match 24.6%; Score 457; DB 4; Length 330;
; Best Local Similarity 34.7%; Pred. No. 4.6e-36;
; Matches 118; Conservative 56; Mismatches 130; Indels 36; Gaps 12;
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; QY 22 PPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW---LVDGQEAENLFPYTRP 77
; DB 6 PSVEFLAPSSKSTSG---GTAALGCLVKDYFPEPTVSNWNSGALTSG---VHTFPAVL-- 57
; QY 78 KREGGQTSLOSEVNITQGWMSNTYTCVHKNNGSIPE-----DSSRKC-----A 123
; DB 58 --QSSGLYSLSVVTPSSS-LGTQTYICNVNKKPSNTKVDKVKPEKSCDKTHTCPPCPA 114
; QY 124 DSNPRGVSAVLSRPSFPD-LFIRKSPITCLVLDLAPSKGTVALTWSRASKPVNHSRTRK 182
; DB 115 PELIGGPSVFLFPKPKDITLMISRTPEVTCVVDVSHDEDEVQPNVYDGVGVHNAKTKP 174
; QY 183 EEKQKNGTTLVTSTLPVGTDRDWIEGETYQCRVTHPHLPRALMRSTTKLPGRKLAPEVYML 242
; DB 175 REEQYNSTYRVVSVLTVLHQDLNGKEYCKVSKNGLPAPIEKTISKAKGQPREPQVYTL 234
; QY 243 PPSPEE-TGTRVTCLIRGYPSEISVQWLFNNEEDHTGHTTRPKQKHGTDTPSPFLY 301
; DB 235 PPSREEMTKNQVSLTCLVKGFYPSDIAVWESNQOPEN--NYKTPPVL--SDGSFFLY 290
; QY 302 SRMLVNSIWEKGNLVTCRVVHEALPGSRTLEKSLIHSAG 341
; DB 291 SKLTVDKSRQQGVFSNVHEALHNHYT-QKSLSLSPG 329
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; Search completed: November 14, 2004, 15:11:02
; Job time : 25 secs
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